

us-09-077-017-1.ry

OM nucleic - nucleic search, using sv model

3307.858 Million cell updates/sec

Title: US-09-077-817-1  
 Perfect score: 1539  
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Scoring table: IDENTITY\_NUC

Searched: 780561 seqs, 21379530 residues

Database : GenEmbl : \*

Word size : 0

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**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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3	853	95.6	1376	9	HSLI13	Y08766 H.sapiens m
4	851	95.3	1369	5	A81220	181220 Sequence 3
5	851	95.3	1382	11	HSU07981	U07981 Human inter
6	237.4	15.4	1525	5	181215	181215 Sequence 1
7	237.4	15.4	1567	12	MMU65747	U65747 Mus musculus
8	52.6	3.4	7218	5	166494	166494 Sequence 14
9	45.4	2.9	2882	35	DDISS2PA	M33862 Dicyostella
10	44.3	2.9	178342	41	AC007435	AC007435 Homo sapi
11	44.1	2.9	100000	9	AC020862	AB020862 Homo sapi
12	43.6	2.8	314303	41	AC006279	AC006279 Plasmodium
13	43	2.8	193482	11	AC0004106	AC0004106 Homo sapi
14	42.4	2.8	2402	1	TCRHSREX6	U15127 Escherichia
15	42.4	2.8	6577	2	AF044502	AF044502 Escherich
16	42.2	2.7	110000	42	AC005103	Continuation (4 of
17	41.6	2.7	43254	36	CELC17E7	AF016643 Caenorhab
18	41.2	2.7	167816	42	AC001947	AC009949 Homo sapi
19	41	2.7	224448	33	AC008464	AL035477 Plasmodium
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21	41	2.7	178896	41	AC0080841	AC0080841 Homo sapi
22	40.8	2.7	196149	34	AC0004709	AC004709 Plasmodium
23	40.8	2.7	172369	42	AC006280	AC006280 Plasmodium
24	40	2.6	2763	3	RAHMNDPA	M22640 Rabbit MHC
25	40	2.6	156373	34	ACU007422	ACU007422 Homo sapi
26	40	2.6	164399	35	PFMA13P6	298551 Plasmodium
27	40	2.6	4773	36	AF003506	AF003506 Plasmodium
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36	39.2	2.5	41628	35	CELC48C5	U03994 Caenorhabd
37	39.2	2.5	177471	41	AC0007446	AC0007446 Homo sapi
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39	38.8	2.5	18124	35	CEU10975	U26373 Caenorhabd
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## A. IGNOMENTS

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12-MAR-1998[illegible]

McGarry  
09/077817 Page 1  
Seg. 1Ds 1-4



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     VERSION      1.0
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     ORGANISM     Homo sapiens
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	DEFINITION	ESU70981 . 1382 bp mRNA	PRI	
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	NID	U70981		
	VERSION	J65J394		
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		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
		Etheria; Primates; Carnivora; Hominiinae; Homo.		
		(Phases I to J382)		
RTTENCE		Donaldson,D.D., Whittiers,M.J., Fitz,L., Neben,T., Finnerty,H.,,		
AUTHORS				

TITLE Henderson, S.L., O'Hara, R.M., Turner, K.J., Wood, C.R. and Collins, M.  
JOURNAL Identification of a third chain for the murine IL-13 receptor  
REFERENCE 2 (bases 1 to 1382)  
AUTHORS Whitters, M.J., Donaldson, D.D., Fitz, L., Neben, T., Finmerly, H. and Collins, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-SEP-1996) Molecular Immunology, Genetics Institute,  
87 Cambridge Park Dr., Cambridge, MA 02140, USA

## FEATURES

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LOCUS

DEFINITION Sequence 1 from patent US 5710023.  
 ACCESSION 181219  
 NID 63209509  
 VERSION 181219.1 GI:3209505  
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 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1525)  
 AUTHORS Collins, M., Donaldson, D., Fitz, L., Neben, T., Whitters, M. and Wood, C.  
 TITLE IL-13 cytokine receptor chain  
 JOURNAL Patent: US 5710023-A 1 20-JAN-1998;  
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 BASE COUNT 505 a 246 c 327 g 447 t  
 ORIGIN

Query Match 15.4% Score 237.4; DB 5; Length 1525;  
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 QY 512 atatacacaagaagaatccagaactaaagtccaagatgaatttggtgagaatgagat 571  
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 DB 625 ATATCAGATGAGAGAGATTTGGAATCAATTCAGCA-----CATGAG 669  
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 QY 752 aggtatgagatcttccctactatggaataaaggagcagtgagcatcagactataaagatt 811  
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 954 TTCCTCATATTAATGATGAGAAATTCATTAATTAATGAATGAATGAGACACCT--- 1021  
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 QY 1112 ccttgaacacacaaagaacccgaataagaagtttttagtgcataatgcttgta 1171  
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 DB 1159 GTAGAGTGAAGTCAATATATTTGTCAGATGATGCAATTTGG 1203

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 DEFINITION  
 ACCESSION U65747  
 NID 93483093  
 VERSION 965747.1 GI:3483093  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Donaldson, D.D., Whitters, M.J., Fitz, L., Neben, T.Y., Finerty, H.,  
 and Collins, M.  
 TITLE The murine IL-13 receptor alpha 2: molecular cloning,  
 characterization, and comparison with murine IL-13 receptor alpha 1  
 JOURNAL J. Immunol. 161 (5), 2317-2324 (1998)  
 MEDLINE 98391042  
 REFERENCE  
 MEDLINE 3 (bases 1 to 1567)  
 AUTHORS Donaldson, D.D., Whitters, M.J., Fitz, L., Neben, T.Y., Finerty, H.,  
 Henderson, S.L., O'Hara, R.M., Turner, K.J., Wood, C.R. and Collins, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JUL-1996) Molecular Immunology, Genetics Institute,  
 87 Cambridge Park Dr., Cambridge, MA 02140, USA  
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 TNYTFMFVEGLDHALQCADYLDHDEKKNVGCISNDSSDYKDFICVNGSSKLEIR  
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BASE COUNT 514 a 249 c 337 g 467 t  
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Query Match 2.9%; Score 44.4; DB 41; Length 178342;  
 Best Local Similarity 49.2%; Pred No 1.5; Matches 117; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

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Oy      955  ttcatgtgaataatgaagctgaagaatggagacataccttgtttagagcgctggaccattccagc 1014
Db 111479  AACATGTTATTGGAAGAGATATGCGCTAGAAATTTTTTAAATATGAAACAACATGTGAGC 111420
Oy      1015  aaggtgttcttgattgaattgaattgagatcagagaatgatgacttaccgaagcatggagga 1074
Db 111419  GACAAATCTTAGAAGAGCTTAGGGAATCCAGAGACATATTAATTTTTTAAAGGCCATGCGTAG 111360
Oy      1075  attgttgagactgcacaggttgaataatgaacatcaccttgaataaacaacatgaa 1132
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RESULT 11
LOCUS      AB020862/c
DEFINITION Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
            hepatocellular colorectal and non-small cell lung cancer , segment
            5/11.
ACCESSION  AB020862
VERSION    g4003382
KEYWORDS   AB020862.1  GI:4003382

SOURCE     Homo sapiens DNA.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (sites)
            Nakamura,Y. and Isumura,M.
            Homo sapiens 1,210,381bp genomic DNA of 8p21.3-p22 anti-oncogene of
            hepatocellular colorectal and non-small cell lung cancer region
            published only in Database (1998) In press
            2 (bases 1 to 100000)
            Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
            Direct Submission
            Submitted (30-NOV-1998) to the DDBJ/EMBL/GenBank databases. Mika
            Hirakawa, Japan Science and Technology Corporation (JST), Advanced
            Database Department: 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028,
            Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491,
            Fax:81-3-5214-8470)
            This sequence is conducted by Japanese Foundation for Cancer
            Research as a JST sequencing team
            Principal Investigator: Yusuke Nakamura Ph.D.
            Phone:+81-3-5449-5372, Fax:+81-3-5449-5433,
            yusuke@ngc.ims.u-tokyo.ac.jp
            The sequence is submitted by:Human Genome Sequencing in ALIS
            project of JST
            Japan Science and Technology Corporation (JST)
            5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site
            (http://www.alis.tokyo.jst.go.jp/HGS/top.html)
            or send email to webmaster@www-alis.tokyo.jst.go.jp.

FEATURES
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Best Local Similarity 63.0%: Pred. No. 2.1:
Matches 68: Conservative 0: Mismatches 40: Indels 0: Gaps 0:
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Dn	63693	GATTTAACCTCAAGTCAAACTCCTTATATGGAAGATATCGTAGAATT	63645
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DEFINITION	Plasmodium falciparum chromosome 12 clone 3D7, WORKING DRAFT SEQUENCE, 16 unordered pieces.		
ACCESSION	AC006279		
NID	95915277		
VERSION	AC006279.4 GI:5919277		
KEYWORDS	HTG; HTGS_PHASEI.		
SOURCE	Malaria parasite P. falciparum.		
ORGANISM	Plasmodium falciparum		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
AUTHORS	1 (bases 1 to 314303) Nyman,R.W., Fung,E.L., Qln,F., Rowley,D., Tamaki,T., Kurdi,O.B., Corway,A.B. and Davis,R.W.		
TITLE	Plasmodium falciparum 3D7 chromosome 12		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 314303) Hyman,R.W., Fung,E.L., Qln,F., Tamaki,T., Kurdi,O.B. and Davis,R.W.		
AUTHORS	Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
TITLE	On Sep 23, 1999 this sequence version replaced gi:4558576. NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
COMMENT			
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*	7842 8041: gap of unknown length		
*	8042 67772: contig of 35731 bp in length		
*	67773 67972: gap of unknown length		
*	67973 142824: contig of 74852 bp in length		
*	142825 143024: gap of unknown length		
*	143025 147294: contig of 4270 bp in length		
*	147295 147494: gap of unknown length		
*	147495 153406: contig of 5312 bp in length		
*	153407 153606: gap of unknown length		
*	153607 161784: contig of 8178 bp in length		
*	161785 161984: gap of unknown length		
*	161985 163895: contig of 1911 bp in length		
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*	177107 177306: gap of unknown length		
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*	179420 179619: gap of unknown length		
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*	237111 237310: gap of unknown length		
*	237311 269228: contig of 31918 bp in length		
*	269229 269428: gap of unknown length		
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Q 1382 aaccuccaccocaaagattccgaattttctgtgatatacatgaagaagattgcatct 1441
Dh 143446 ATTCATCTCTGTAATAATATTCATGAAAGTTTTCATGTCACGACAGACATTTGAATTA 143505

O 1442 ttc 1444
Dh 143506 TTC 143508

RESULT 14
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LACUS Escherichia coli extended core protein Rhes and ORF f202 genes,
DEFINITION partial cds, and unidentified ORF, complete cds.
ACCESSION U05127
VERSION U05127.1 GI:563992
KEYWORDS 6 of 6
SOURCE Escherichia coli.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
REFERENCE 1 (bases 1 to 2402)

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**AUTHORS** Zhao, S. and Hill, C.W.  
**TITLE** Reshuffling of Rhs components to create a new element  
**JOURNAL** J. Bacteriol. 177 (5), 1393-1398 (1995)  
**MEDLINE** 95173120  
**REFERENCE** 2 (bases 1 to 2402)  
**AUTHORS** Hill, C.W.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (26-SEP-1994) Charles W. Hill, Biochemistry



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4	840	54.6	1269	1	T96782	Human zcytoz2 cyto	
5	830	53.9	1288	1	V04075	Human cytokine/pep	
6	830	53.9	1288	1	V02295	Human sapiens cDNA	
7	830	53.9	1288	1	V04331	Human HR-1 recept	
8	727.2	47.3	1167	1	T96783	Human zcytoz2 cyto	
9	624	40.5	1136	1	T96784	Celebs macaque zyt	
10	595	38.7	1079	1	V22701	Construct containi	
11	595	38.7	947	1	V22702	Construct containi	
12	287	18.6	436	1	V89756	Mature interleukin	
13	242.4	15.8	465	1	T22698	EST clone CS520. N	
14	237.4	15.4	1525	1	T95213	Interleukin-13 bin	
15	221.6	14.4	473	1	V22697	CDNA encoding the	
16	36	2.3	2398	1	O65354	Interleukin-13 bin	
17	36	2.3	1618	1	V74914	Outer membrane 1lf	
18	35.8	2.3	110000	1	V21309_14	Staphylococcus au	
19	35.8	2.3	222	1	V90526	Continuation (15 c	
20	35.8	2.3	1721	1	X07566	EST clone BK384. N	
21	35	2.3	110000	1	V21309_11	Homo sapiens Tetap	
22	35	2.3	116624	1	V52850	Continuation (12 c	
23	34.6	2.2	10023	1	T68933	Human eyal gene ce	
24	34.6	2.2	6810	1	X20267	Bovine P17-1 exon	
25	34.6	2.2	7439	1	N91312	Borrelia burgdorfi	
26	34	2.2	7502	1	O27429	PCN11 plasmid. Sym	
27	34	2.2	110000	1	T58840_4	PCPD. PCPD plasmid	
28	33.8	2.2	110000	1	V21309_09	Continuation (5 o	
29	33.8	2.2	3704	1	V54590	Continuation (10 c	
30	33.8	2.2	812	1	X39990	Human secretory pr	
31	33.6	2.2	6124	1	O03568	Prostate cancer as	
32	33.4	2.2	10357	1	V52324	Sequence encoding	
33	33.4	2.2	1532	1	X00641	Streptococcus pneu	
34	33	2.1	110000	1	V21309_06	Human secreted pro	
35	32.8	2.1	8805	1	X13072	Continuation (7 o	
36	32.6	2.1	237326	1	V57803	Enterococcus faec	
37	32.6	2.1	6234	1	V74715	Hereditary haemoch	
38	32.6	2.1	45546	1	X23520	Staphylococcus au	
39	32.4	2.1	1265	1	O26097	Human kidney amin	
						MIG-1. New monokl	

RESULT	1
185826	
ID	785826 standard; DNA; 1539 BP.
AC	785826
DT	22-JUN-1998 (first entry) *
DE	Human Interleukin-13 beta receptor DNA.
KW	Interleukin-13 receptor; inflammation; allergy. IL-13; ss.
OS	Homo sapiens.
PN	W09720926-A1
SD	12-JUN-1997
DE	07-NOV-1996; F01756.
DE	06-DEC-1995; FR-014424.
FA	(SNFI) SPNOFI SA.
PC	Caput D. Garrara P, Laurent P, Vita N;
ER	WPI; 97-19773/29.
DR	P-FSDB; 924572.
PT	New purified human interleukin-13 receptors -
FT	acidic, useful for diagnosis and treatment of inflammation, allergy,
ET	etc
SS	Claim 6; Figes 41-42; 83pp; French

CC This sequence encodes human interleukin-13 (IL-13) beta receptor. The  
CC Invertor: relates to new purified peptides comprising 380 or 427 amino  
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
CC affinity. But acquires high affinity when associated with the IL-4  
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as  
CC diagnostic probes to identify aberrant synthesis or genetic anomalies  
CC such as loss of heterozygosity and rearrangements, or chromosomal  
CC anomalies. They are also used for production of recombinant IL-13R beta  
CC and alpha which can be used as IL-13 antagonists, specifically to  
CC regulate IL-13-induced responses for treatment of inflammation and  
CC allergy. IL-13 receptors are also useful as antisense molecules for gene  
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard  
CC immunoassays) to diagnose diseases associated with abnormal expression  
CC of IL-13 receptors. When coupled to a toxin also for treatment of  
CC overproduction of IL-13R. Cells that express IL-13R at the surface are  
CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta  
CC is encoded by the nucleic acid sequence shown in Figure 2a in the  
CC specification (T864664), which is not the same as that shown in the  
CC sequence listing (T85626).

Query Match	100.0%	Score 1539;	DB 1;	Length 1539;
Best local Similarity	100.0%	Pred. No. 0;		
Matches 1539;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	gfgbcbctgctgcgcggagagagcaatatacaaggttttaactcgtgagaaabtggtta	60
Dy	1	gcbhccctctgcgcggagagagcaatatacaaggttttaactcgtgagaaabtggtta	60
Qy	61	atccgtttgcttggtctatcgatgcttataaaccttctgataagacaacaacattggtcg	120
Dy	61	attcgtttgcttggtctatcgatgcttataaaccttctgataagacaacaacattggtcg	120
Qy	121	tacaagcttttgcaattcatcttcacaagacacggatataaaggttaacccctctcagaattt	180
Dy	121	taaaagcttttgcaattcatcttcacacacggatataaaggttaaacccctctcagaattt	180
Qy	181	tgagatgagggatattgaagaagaaacccgataacttaagtatcctcatttgcaattggcaa	240
Dy	181	tgagatgagggatattgaagaagaaacccgataacttaagtatcctcatttgcaattggcaa	240

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QY      1321   gtttattcttatattagtgtatatacttgtaacggcgttcgtagtgaatgltgcgaaacc 1380
D1       1321   GTTTATCTTATTATATAGTATATATTTGTAAACCGGTCGCTGGTAGTGTAATGTTCCGAACCC 1380
QY      1381   aaaccaccaccacaataatgatccagaattttctcttgtataatgaagaagattgcac 1440
D1       1381   AAACACCTAACCAAAAANATGCATGCCAATTTTCTCTGTATACATGAAGAAGATTGGCATC 1440
QY      1441   ttccatcatcaagagacatcggtattgactaacaggtlccagtcacgcccgaatgtcaa 1500
D1       1441   TTCCCATATCAAGAGACATGATGATGACTCAACAAGCTTTCCAATCATGCCCCAAATGTTCAA 1500
QY      1501   tatgagtcataaatgaattttcttcgcaagtgtg 1539
D1       1501   TATGAGTCTCATATAACTGAATTTTTCTTCCGAAGTTGG 1539

RESULT    2
ID         1      ID86464 standard; DNA; 1298 bp.
AC         1      AC86464;
AD         1      AD86464;
DE         1      DE22-JUN-1998 (first entry)
KW         1      KWHuman interleukin-13 beta receptor DNA.
FH         1      FHInterleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss.
FT         1      FTKey
FT         1      FTDNA
FT         1      FTCDSDS
          1      Location/Qualifiers
          1      53..1195
          1      /tag= a
          1      /product= IL-13_beta_receptor
          1      MO9720926-A1
PD         1      PD12-JUN-1997.
PE         1      PE07-NOV-1996; F01756.
PR         1      PR06-DEC-1995; FR-014424.
PA         1      PA(SNFI ) SANOFI SA.
DR         1      DRCaput D, Ferrara P, Laurent P, Vita N;
           1      MPI: 97-319773/29.
           1      P-PDB: W24972.
PT         1      PTNew purified human interleukin-13 receptors - and related nucleic
PT         1      PTacids, useful for diagnosis and treatment of inflammation, allergy,
PT         1      PTetc
PS         1      PSClaim 6; Figure 2a; 83pp; French
CC         1      CCThis sequence encodes human interleukin-13 (IL-13) beta receptor. The
CC         1      CCinvention relates to new purified peptides comprising 380 or 427 amino
CC         1      CCacid sequences, which are receptors for interleukin-13 (IL-13); the 380
CC         1      CCand 427aa proteins are designated IL-13R beta and alpha respectively.
CC         1      CCThe IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
CC         1      CCaffinity, but acquires high affinity when associated with the IL-4
CC         1      CCreceptor. Nucleic acids encoding IL-13R beta and alpha are used as
CC         1      CCdiagnostic probes to identify aberrant synthesis or genetic anomalies
CC         1      CCsuch as loss of heterozygosity and rearrangements,, or chromosomal
CC         1      CCanomalies. They are also used for production of recombinant IL-13R beta
CC         1      CCand alpha which can be used as IL-13 antagonists, specifically to
CC         1      CCregulate IL-13-induced responses for treatment of inflammation and
CC         1      CCallergy. IL-13 receptors are also useful as antisense molecules for gene
CC         1      CCtherapy (blocking synthesis of IL-13R). Antibodies are used (in standard
CC         1      CCimmunoassays) to diagnose diseases-associated with abnormal expression.
CC         1      CCoverproduction of IL-13 receptors, when coupled to a toxin also for treatment of
CC         1      CCused to identify ligands and modulators of IL-13R at the surface are
CC         1      CCis encoded by the nucleic acid sequence shown in Figure 2a in the
CC         1      CCSpecification (T86464), which is not the same as that shown in the
SC         1      SCsequence listing (T85826).
SQ         1      SQSequence 1298 BP: 407 A; 231 C; 266 G; 394 T;

Query Match      55.7%; Score 857; DB 1; Length 1298;
Best Local Similarity 84.3%; Pred. No. 4,5e-224;
Matches 1298; Conservative 0; Mismatches 0; Indels 241; Gaps 20.

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QY 61 atccgttcttgatcgcagatgattatatactcttctgataaagcaacatttgctg 120  
 |||||  
 DB 59 -ttcgttcttgatcgcagatgattatatactcttctgataaagcaacatttgctg 117  
 |||||  
 QY 121 taacagcttcttgatcgcagatgattatatactcttctgataaagcaacatttgctg 180  
 |||||  
 DB 118 t-----actcattctcagacacagagatgataaagcaacatttgctg 165  
 |||||  
 QY 181 tgcagatagatgattatatactcttctgataaagcaacatttgctg 240  
 |||||  
 DB 166 tgcagatagatgattatatactcttctgataaagcaacatttgctg 214  
 |||||  
 QY 241 ccccccctctcttgatcgcagatgattatatactcttctgataaagcaacatttgctg 300  
 |||||  
 DB 215 ccccccctctcttgatcgcagatgattatatactcttctgataaagcaacatttgctg 265  
 |||||  
 QY 301 aaatccgcaaacatttgatgataaagcaacatttgctg 360  
 |||||  
 DB 266 aaatccgcaaacatttgatgataaagcaacatttgctg 310  
 |||||  
 QY 361 aaatccgcaaacatttgatgataaagcaacatttgctg 420  
 |||||  
 DB 311 aaatccgcaaacatttgatgataaagcaacatttgctg 360  
 |||||  
 QY 421 gaagatacagccttcttgatgataaagcaacatttgctg 480  
 |||||  
 DB 361 gaagatacagccttcttgatgataaagcaacatttgctg 419  
 |||||  
 QY 481 tgcagatagatgattatatactcttctgataaagcaacatttgctg 540  
 |||||  
 DB 419 -----tgcagataaacatttgatgataaagcaacatttgctg 468  
 |||||  
 QY 541 agtccgcaaacatttgatgataaagcaacatttgctg 600  
 |||||  
 DB 469 agtccgcaaacatttgatgataaagcaacatttgctg 513  
 |||||  
 QY 601 ctgtcttgataaacatttgatgataaagcaacatttgctg 660  
 |||||  
 DB 514 ctgtcttgataaacatttgatgataaagcaacatttgctg 559  
 |||||  
 QY 661 aactcttgataaacatttgatgataaagcaacatttgctg 720  
 |||||  
 DB 560 aactcttgataaacatttgatgataaagcaacatttgctg 605  
 |||||  
 QY 721 tgcagatagatgattatatactcttctgataaagcaacatttgctg 780  
 |||||  
 DB 606 tgcagatagatgattatatactcttctgataaagcaacatttgctg 659  
 |||||  
 QY 781 agtccgcaaacatttgatgataaagcaacatttgctg 840  
 |||||  
 DB 659 -----gagcattcagcatttgatgataaagcaacatttgctg 709  
 |||||  
 QY 841 aactcttgataaacatttgatgataaagcaacatttgctg 900  
 |||||  
 DB 710 aactcttgataaacatttgatgataaagcaacatttgctg 756  
 |||||  
 QY 901 agtccgcaaacatttgatgataaagcaacatttgctg 960  
 |||||  
 DB 757 agtccgcaaacatttgatgataaagcaacatttgctg 807  
 |||||  
 QY 961 tgcagatagatgattatatactcttctgataaagcaacatttgctg 1020  
 |||||  
 DB 808 tgcagatagatgattatatactcttctgataaagcaacatttgctg 858  
 |||||  
 QY 1021 tgcagatagatgattatatactcttctgataaagcaacatttgctg 1080  
 |||||  
 DB 859 tgcagatagatgattatatactcttctgataaagcaacatttgctg 901  
 |||||  
 QY 1081 gtcagatagatgattatatactcttctgataaagcaacatttgctg 1140  
 |||||  
 DB 902 gtcagatagatgattatatactcttctgataaagcaacatttgctg 959  
 |||||

QY 1141 atnagcttcttgatgataaacatttgatgataaagcaacatttgctg 1200  
 |||||  
 DB 959 -----caattatgcttcttgatgataaacatttgatgataaagcaacatttgctg 1002  
 |||||  
 QY 1201 agatcagatgatttgatgataaacatttgatgataaagcaacatttgctg 1260  
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 DB 1003 agatcagatgatttgatgataaacatttgatgataaagcaacatttgctg 1048  
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 QY 1261 gtcagatagatgattatatactcttctgataaagcaacatttgctg 1320  
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 DB 1049 gtcagatagatgattatatactcttctgataaagcaacatttgctg 1097  
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 QY 1321 gtcagatagatgattatatactcttctgataaagcaacatttgctg 1380  
 |||||  
 DB 1095 gtcagatagatgattatatactcttctgataaagcaacatttgctg 1149  
 |||||  
 QY 1361 aacacccaccccaaacatttgatgataaacatttgatgataaacatttgctg 1440  
 |||||  
 DB 1150 aacacccaccccaaacatttgatgataaacatttgatgataaacatttgctg 1199  
 |||||  
 QY 1441 ttcagatagatgattatatactcttctgataaagcaacatttgctg 1500  
 |||||  
 DB 1200 ttcagatagatgattatatactcttctgataaagcaacatttgctg 1259  
 |||||  
 QY 1501 tatgagctcagatgattatatactcttctgataaagcaacatttgctg 1539  
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 DB 1260 tatgagctcagatgattatatactcttctgataaagcaacatttgctg 1298  
 |||||

RESULT 3  
 T55214  
 ID T55214 standard; cDNA; 1369 BP.  
 AC T55214;  
 DE 27-MAR-1998 (first entry)  
 KW Interleukin-13; IL-13; Interleukin-13 receptor binding chain; IL-13c;  
 KW mediator; IL-13 receptor binding inhibition; IGF-mediated condition;  
 KW allergy; asthma; immune complex disorder; ds.  
 OS Homo sapiens.  
 FU Key  
 FT CDS location/Qualifiers  
 FT 103..1245  
 FT sig\_peptide /\*tag- a  
 FT 103..117  
 FT /\*tag- b  
 FT mat\_peptide /\*tag- c  
 FT 178..1242  
 FT 103..1245  
 PN WO9731946-A1.  
 PD 04-SEP-1997.  
 PE 28-FEB-1997; U03124.  
 PR 01-MAR-1996; US-609572.  
 PL (GENE) GENETICS INST INC.  
 PI COLLINS M, Donaldson D, Filtz L, Neben T, Whittens M,  
 PI Wood C,  
 PI MPI: 97-418632/41.  
 DR P-PSDB; W35295.  
 PT New nucleic acid encoding Interleukin-13 receptor binding chain and  
 PT transformed cells - proteins, antibodies and inhibitors, for  
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
 PT and in diagnosis  
 PS Claim 1; Pages 32-33; 49pp; English.  
 CC The present sequence encodes the human interleukin-13 (IL-13) binding  
 CC chain of the interleukin-13 receptor, designated IL-13c. IL-13c acts a  
 CC mediator of the known biological activities of IL-13. The present  
 CC sequence was isolated from human testis library. Recombinant  
 CC IL-13c proteins, and antibodies raised against them, are used to  
 CC inhibit the binding of IL-13 to its receptor. They are particularly used  
 CC to treat IGF-mediated conditions, e.g. allergy, asthma and immune complex  
 CC disorders, especially lupus, nephritis, thyroiditis and Graves' disease.  
 CC They are also used to treat immune deficiency (particularly in  
 CC hematopoietic progenitor cells), cancer etc., and to increase macrophage  
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  
 CC with such activity is combined with IL-13c and the mixture applied,  
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor





PR 12-JUN-1996; US-017843.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 PI Appelbaum ER, Hu J.  
 DR P-PSDB: W41502.  
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to  
 PT increase resistance to infections in individuals with trauma and/or  
 PS burns  
 PS Claim 4: Page 26-27; 34pp: English.  
 CC This cDNA clone codes for a novel human cytokine/peptide hormone  
 CC receptor, designated HR-1 receptor (see W41502). Plasmid ATG-531,  
 CC comprising HR-1 receptor cDNA contained in vector Bluescript SK+,  
 CC is deposited in E. coli JM101 as ATCC 98069. The clone was  
 CC isolated from a human testis cDNA library. Also claimed are a  
 CC polypeptide comprising amino acids 1-380 or 22-380 of the 380  
 CC residue HR-1 receptor amino acid sequence, a vector comprising  
 CC polypeptide, antibody against the polypeptide, an agonist to the  
 CC that inhibits the activity of the polypeptide, HR-1 receptor  
 CC protein and polynucleotides can be used for research, biological,  
 CC diagnosis and (gene) therapy applications, e.g. to increase  
 CC resistance to infections in individuals with trauma and/or burns,  
 CC and to prevent, ameliorate, treat, diagnose and/or determine  
 CC predisposition to asthma, allergic disorders or disorders of  
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or  
 CC cyclic neutropenia or as a consequence of cytotoxic therapy of  
 CC cancer. Lymphoma, leukaemia and/or Bone marrow transplantation.  
 SO Sequence 1288 BP; 421 A; 227 C; 252 G; 388 T;

Query Match 53.9% Score 830; DB 1; Length 1288;  
 Best Local Similarity 84.1%; Pred. No. 1e-216;  
 Matches 1271; Conservative 0; Mismatches 0; Indels 241; Gaps 20;

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OY 23 ggcaatcaagaagtttaactctcggagaaatggcttaattcgttcttgatcgaaga 82
DB 1 GGCATATCAAGGTTTAAATCTCGAGAAATGCT--TTCGTTCTTGGCATATGGA 57
OY 83 tgcctatataccttctcgtatagaacaaactttgctgtaagaactttgcaactcct 142
DB 58 TGTATTATACCTTCTGATAGACAAACATTTGGCTGT-----ACTTCATCT 105
OY 143 tcaaacaccgagataaaagttaacctccacaggaatttagatagatagatagaag 202
DB 106 TCAACACCCGAGATAAAGTTAACCCCTCAGAGATTTAGATAGTGAAT----- 157
OY 203 aaccggatacttaggttattctatatttgaaggaaccccaactgtctcgtgacatt 262
DB 157 -CCCGGATTAAGTATCTATCTATTTCATAGGCAACCCCACTGCTCTGATCATT 214
OY 263 ttgtgtgtgtaaaaggaatgacagttgaaatgaaataacgaacatttggaag 322
DB 215 TT-----AAGGATGACACAGTGAATATGAATAAATCCGAACATTTGGTAGG 265
OY 323 aaacatggaagtagttagaggtacatacttacttaagaacttacttaagaatg 382
DB 266 AACATGAGAG-----ACCATATTACTTAAGATCTACTATCAAAAGATG 310
OY 383 ggtttgattcttaacaaggcatgaaatagaaaggcgaagatacaacgcttttaca 442
DB 311 GGTTTGATCTTAACAAGGCGATTGAA-----GCCAATATACACACGCTTTTACCA 360
OY 443 tggcaatgacaaatgagatcagaagtccaagtccaagtccaagtccaagtccaagt 502
DB 361 TGGCAATGCAAAATGAGATCAGAAATCAAAAGTTCC-----TGGCGAAGAACT 408
OY 503 acttattgataatcaacaagaagaaatccagaactaaagtccaagtccaagtccaagt 562
DB 409 ACTTATTGATATCAACCAAGGATTCAGAACTAAAGTTTCAGAT----- 457
OY 563 agaagattcgttatatacaattggaataattactctgttcttggaaacctggcata 622

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DB 457 ---ATGATTCGGATATATTACAAATTGCGAATATTACTGTTCTTGGAAACCTGGCANA 513
OY 623 ggttaactatgctcgtggaactctctgtataccaattacaactgttttactgtatgaag 682
DB 514 GGT-----GTACTTCTTATACCAATTATCAAACTGTTTACTGATATGAGG 559
OY 683 gcttggaatcagcatataataatttgaaacagtggtgtgattacatacaagctgtag 742
DB 560 GCTTGATATCAGCAAT-----ACAGTGTGTTGATTATCATCAAGGCTGATGG 605
OY 743 acaaatatagatgacagattccctatttgcacaataaaggagcagtgagcagcagat 802
DB 606 ACAAATATGAGATGACGATTTCCCTATTGG-----GAGCATACAGCT 649
OY 803 ataaagttctctatattgtgtgtaagatcatcagaagacaagcctgaaataatcaaga 862
DB 650 ATAAAGATTCTATATTGTTGTTAATGATCATCAAGAAACAGCT----- 697
OY 863 atcagatcagattattcacttctcagttccaataatatagttaaaccttggccagct 922
DB 697 ATCAGATCCAGTATTTCACCTTTTACGCTCAAAATATAGTTAACTTTGCCGCACTC 756
OY 923 agtggaaatctctcttcttctcgtggaggttcaigtgaataaagctgaaatgagc 982
DB 757 -----TACTTACTTTTACTCGGAGAGCTTATGTAATTAACCTGAATATGAGC 807
OY 983 atacctgtttagagcgttgagacatctccagaaggtgtttgttataagaattgagatc 1042
DB 808 ATACCTTTG-----GGACCTATTCACGAAAGCTTTTGTATATGAATATGAGATC 858
OY 1043 agagaagaatgatacaccgaatgacatgaggaatattggtacgtctacagttgaaatg 1102
DB 859 AAGAGAGATGATATAC-----TTGGTACTGCTACAGATTGAATG 901
OY 1103 aaacataccttgaacaaacaaatgaaacccgaataatagattttagtgaacta 1162
DB 902 AAACATACACCTTGAACAAATCAATGAACCCCA-----CAATTA 942
OY 1163 tgccttgaagaagaagaagtgaataatttgcacagatgacggaatttggcgaag 1222
DB 943 TGCCTTGAAGAAAGCAAGTAATTTATTTGTCACATGACGGAATTTGG----- 997
OY 1223 aatcaagtagtgaatgagatgaataacaatgctgggaagttgaaagcctatcgaagaaa 1282
DB 997 -----AGTGAATGAGATGAATAAATGCTGGAGGAGTGAAGACCTATGCAAGAAAA 1048
OY 1283 ctgttgatagtcgtggaatcgttctcgtacatttggtttcaatcttaattagttat 1342
DB 1049 CTTTGCTA-----CGTTCTGGCTACCATTTGGTTTCATCTTAATATTAGTTAT 1097
OY 1343 attgtaacggctcgtttagtgaatggttgcgtaagcacaacccatccacaataatgatt 1402
DB 1098 ATTGTGAACGGCTGTGTT-----TTGCGTAAACCAACCACTTACCCAAAAATGATTT 1149
OY 1403 ccagaatttctgtgatacagaagaagatttgcattcttccatatacaagaagatgatt 1462
DB 1150 CCAAGAAATTTTCTGATATCATGAGAA-----CTTTCATATCAAGAGCATGAT 1199
OY 1463 attgactcaacagtttcagttatgagccaaatggttcaataatgagttcaataatgatt 1522
DB 1200 ATTGATTCAGAACTTTCCAGTATGCGCAAAATGTTCAATATGAGTCTCAATTAACCTGAAAT 1259
OY 1523 ttttcttgcgaa 1534
DB 1260 TTTTCTTGGAA 1271

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RESULT 6  
 IL V02295 standard; cDNA; 1288 BP.  
 AC V02295;  
 DT 08-JUN-1998 (first entry)  
 DB Homo sapiens cDNA encoding the HR-1 receptor.



OY 1523 ttcttcgcga 1534  
 DB 1260 TTTCTTGGCA 1271

RESULT 7  
 V04131  
 ID V04131 standard; cDNA; 1288 BP.  
 AC V04131;  
 DT 22-JUN-1998 (first entry)  
 DE Human HR-1 receptor cDNA.  
 KM HR-1 receptor; human; cytokine; infection; asthma; allergy;  
 OS haematopoietic disorder; therapy; diagnosis; ss.  
 FH Homo sapiens.  
 FT Key Location/Qualifiers  
 FT CDS 31..1173  
 FT sig\_peptide /tag- a  
 FT /tag- b  
 FT mat\_peptide 94..1170  
 FT /tag- c  
 FT /note- "(Claim 5)"

WO9747741-A1.  
 18-DEC-1997.  
 12-JUN-1996; U10262.  
 12-JUN-1996; WO-010262.  
 (HUMA-) HUMAN GENOME SCI INC.  
 (SMIK) SMITHKLINE BEECHAM CORP.  
 Appelbaum ER, Hu J;  
 WPI: 98-052308/05.  
 P-PSDB: W41520.

Nucleic acid sequence encoding human cytokine peptide hormone  
 Receptor - useful to treat, prevent or diagnose, e.g. lowered  
 resistance to infection, asthma, allergy or haematopoietic disease  
 Claim 4; Page 61-62; 76pp; English.  
 This cDNA clone, deposited as ATCC 98069, codes for a novel human  
 cytokine/peptide hormone receptor, designated the HR-1 receptor  
 (see W41520), that shows homology to the interleukin-5 receptor.  
 The 1288 bp sequence was isolated from a human testis tissue  
 library. The isolated clone can be used for the recombinant  
 production of HR-1 receptor, as a source of probes to isolate  
 genomic HR-1 receptor clones, as a source of PCR primers, as a  
 diagnostic reagent (particularly to detect gene mutations which  
 may indicate susceptibility to disease), for chromosome  
 identification and mapping, and in a claimed method for treating  
 a patient having need of HR-1 receptor. HR-1 receptor activators  
 and agonists can be used to treat, prevent or diagnose  
 predisposition to lowered resistance to infection, asthma, allergic  
 or haematopoietic disorders, e.g. where induced by AIDS, aplastic  
 anaemia, neutropenia or cytotoxic treatments for cancer.  
 Sequence 1288 BP; 421 A; 227 C; 252 G; 388 T;

Query Match 53.9%; Score 830; DB 1; Length 1288;  
 Best local similarity 84.1%; Pred. No. 1e-216;  
 Matches 1271; Conservative 0; Mismatches 0; Indels 241; Gaps 20;

OY 23 ggcacatataaaggtttaactcgcgagaaatggtcttaattgttgcctgcgcga 82  
 DB 1 GGCACATATCAAGTTTAAATCTCGAGAAATGGCT--TTGGTTGCTGGCTATCGGA 57  
 OY 83 tgcctatataccttctcgtataagcaaacattggtcgtlacaagcttttgcactcatc 142  
 DB 58 TGCCTATATACCTTTCTGTAAGCAACATTTGGCTG-----ACTTCACT 105  
 OY 143 tcaagacacgagataaaagttaacccctcctcagagatttttgagatagtgatgaag 202  
 DB 106 TCAGACACCGAATATAAAGTTAACCTCTCAGATTGAGATAGTCAT----- 157  
 OY 203 aaccggaacttaagtatctctatcttgcaatggaaccccccacatgctcttgatcatt 262  
 DB 157 --CCCGATACTAGTATGCTATCTGATTGCAATGCAACCCCACTGCTCTGATCATTT 214

OY 263 ttgcttgtaaggaatgacacagtggaatataactaaataccgaacattggtagt 322  
 DB 215 TT-----AAGATATGACAGATGGAATATGAACTTAATAATCCGAACATTGGTAGTG 265  
 OY 323 aaacatggaaggtagtagtaggttacccalcactactaagaatctacatcaagaatg 382  
 DB 266 AAACATGGAAG-----ACCATCATTTCTAAGATCTACATTTCAAGATG 310  
 OY 383 ggtttgacttcaagaaggatgtgaattatagaaggcgaagatcacacgctttacca 442  
 DB 311 GCTTATGATCTTAACAAGGCAATTGAA-----GCCAATATCACACGCTTTTACCA 360  
 OY 443 tggcaatgcacaaatggaatgaagaagtcacaagtcccaattgctagtagggcacaact 502  
 DB 361 TGGCAATGCACAAATGATGATCAGAAAGTTCAAAAGTTCC-----TGGCAGAAACT 408  
 OY 503 acttattggtatcacccacaaaggaatccagaactaaagttcaggaattagtttggt 562  
 DB 409 ACTTATGATATCACACCAAGGAATTCAGAAACTAAAGTTCAAGAT----- 457  
 OY 563 agaatggttcgtatattacaaattggcacaatatctctgtcttgaaacctggcata 622  
 DB 457 --ATGATTTGGTATATATACAAATGGCAATTTACTCTGTTGAAACCTGGGATA 513  
 OY 623 ggttactatattctcgggtactcttgatbaaccaattacaacttgttactggtatgag 682  
 DB 514 GGT-----GTACTCTTGATACCAATTACAACTGTTTACTGATATAGG 559  
 OY 683 gcttgatcatgcatataatatttggaacagtggttgaatcatcaagctgtagt 742  
 DB 560 GCTTGATCATCATTT-----ACAGTGTGATATATCAAGGCTGATAGG 605  
 OY 743 acaaatataggaatgcagattccctatttggcaataaagaagcagtgagcagcagact 802  
 DB 606 ACAAATATAGATGATCAAGATTTCCCTATTG-----GAGGATCAAGACT 649  
 OY 803 ataaagattcctataattgttgaattatgataatcaagaagaacagcctgaatatcaaga 862  
 DB 650 ATAAAGATTTCTAATATTTGTTATGATGATCAGCAAGCAAGCC----- 697  
 OY 863 atcagatcagatttcaacttccacttccacgttcaaaatagtttaaccttgcgcgacgc 922  
 DB 697 ATCAGATCACTATTTACACTTTTACACTTCAAAATATGTTAACTTTGCCGCAAGTC 756  
 OY 923 agtggaaatacttacttacttactcggagagatcattgtaaatgaatgaatgagc 982  
 DB 757 -----TATCTTACTTTTACTCGGAGAGTTCATGTAATTAAGCTGAATATGAGAC 807  
 OY 983 atacttggtttagcgctggaccattccagcaaggtgtttgattatagaattgagac 1042  
 DB 808 ATACCTTTG-----GACCTATTTCCAGCAAGGTGTTGATTATGAATTTGAGATC 858  
 OY 1043 agagaagatgatactaccgaaagcatggaagaaatttggtagctgacagttgaaatg 1102  
 DB 859 AGAAGATATATCTATCTCC-----TTGGTGACTGCTACAGTTGAATG 901  
 OY 1103 aaatatcaccttggaaacaaacaaatgaaacccgaataatagaagtttttagtaagaat 1162  
 DB 902 AAACATATCACTTTGAACAAACAAATGAATGAACCGA-----CAATTA 942  
 OY 1163 tgcctttagtaagaagcaagltgaatatlttgtcagatgacggaatttggcagaag 1222  
 DB 943 TGCCTTGTAGTAGAAGCAAGTGAATATTATTTCCTCAGATGACGGAATTTGG----- 997  
 OY 1223 aatcaagtgtagtagtagtagtaaaacatgctgggaagtggaagaccatcagaagaaa 1282  
 DB 997 -----AGTAGTGTGAGTGAATAACAATGCTGGAAGGTGAACACTATCAGAAAGAAA 1048  
 OY 1283 ctgtgtagtaagtagtagctgttctggtacacatttggttcacttaataatagttat 1342  
 DB 1049 CTTTGCTA-----CGTTTCTGCTACCAATTTGGTTCACTTAATATTAATTAT 1097



Query Match	Best Local Similarity	Matches 1137	Conservative	Score 727.2	DB 1	Length 1167
	83.1%	0	Mismatches 3	Pred. No. 9.6e+189	Indels 228	Gaps 18
0Y 1343	attgtcaacggctctgcttagtgaatgtgtgctgaagccaacacccaccacaaaatgatt	1402				
Db 1098	ATTGTGAACGGCTGCTT-----TTGGCTTAAGCCAAACCACTCCAAAAATGATT	1149				
0Y 1403	ccagaattttcttgatcatcatgaagaagatttgcattcttcacatacaagaagatgct	1462				
Db 1150	CCAGAAATTTTCTGTGATCATGAGA-----CTTCCATATCAAGAGACTGGT	1199				
0Y 1463	attgactcaacagtttccagtcattgagccaatggttcaataatgagtcataaactgaat	1522				
Db 1200	ATTGACTCAACAGTTTCCAGTCATGCGCCAAAGTTCAATATGAGTCTCATTAACGTAAT	1259				
0Y 1523	ttttcttgagaa 1534					
Db 1260	TTTTCTTGCGAA 1271					
RESULT 8						
796783						
ID 796783	standard; cDNA: 1167 BP.					
AC 796783						
DT 30-MAR-1998	(first entry)					
DE Human zcytor2 cytokine receptor cDNA.						
KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;						
KM infertility; antagonist; contraceptive; diagnostic; therapeutic; ds.						
OS Homo sapiens.						
FT Key	Location/Qualifiers					
FT CDS	10..1152					
FT /tag= a						
FT /product= zcytor2						
FT /note= "cytokine receptor"						
PN MO9733913-A1.						
PD 18-SEP-1997.						
PE 12-MAR-1997; U04043.						
PF 13-MAR-1996; US-013345.						
PA (Zymo ) ZYMOGENICS INC.						
PI Baumgartner JM, Farrah TM, Foster DC, Grant FJ,						
PI OHara PJ,						
DR WP1: 97-470820/43.						
DR P-PSDB: W36614.						
PT New nucleic acid encoding testis-specific cytokine receptor - useful						
PT for identification of ligands or antagonists, potentially for use as						
PT male contraceptives or for infertility treatment						
PS Claim 2; Page 49-51; 79pp; English.						
CC This sequence encodes a novel ligand-binding receptor, zcytor2, which						
CC shares homology with cytokine receptors and was isolated from a human						
CC testis cDNA library. The resulting polypeptide is a receptor for						
CC cytokines (particularly interleukin-13) and is expressed on the surface						
CC of testicular cells, probably being involved in spermatogenesis. It can						
CC be used to detect ligands that promote proliferation and/or						
CC differentiation of such cells in cultures and may also be used to treat						
CC infertility. Antagonists of this receptor may be used to characterize						
CC ligand-receptor interactions and as male-specific contraceptives. By						
CC blocking the action of IL-13, receptor antagonists and ligand-binding						
CC this receptor can also be used to modulate immune function, e.g. in						
CC allergy and asthma, as a diagnostic to determine circulating levels of						
CC ligand and also to isolate and purify ligands. Antibodies can be used to						
CC assay circulating receptor (an abnormal level may be indicative of						
CC disease such as cancer), for labelling cells that express the receptor,						
CC and therapeutically as antagonist.						
SQ Sequence 1167 BP; 365 A; 213 C; 233 G; 356 T;						

Db	76	-----ACTCATCTTCAGACACCGAGATTAAGGTTAAACCCCTCCAGGATTTT	123
Cy	182	gaggaagggatataagaagaacccggataactaaggtatctctatttgcaatggcaac	241
Dc	124	GAGATATATGGAT-----CCCGGATACTAGGTTATCTTATTTGGCAATGGCAAC	172
Cy	242	ccccacgtctcttgatcatcttgtgtgtgaagaagatgcacagtggaatgtgacaa	301
Cb	173	CCCCACGTCTCTGGATCATTTT-----AAGAAATACACAGGAGATATGACATPA	223
Cy	302	aataccgaacattggtgagtgaacaatggaggtgtagttagaggtttaccatctacta	361
Cb	224	AATACCAACATATTGGATGAGAAACATGGAG-----ACCATCATTTACTA	268
Cy	362	agatctacattacaagaatgggtttgatcttacaagggtctgaattagaaaggcg	421
Cb	269	AGTACATTAACAAAGATGGGTGTGATCTTTAACAAAGGCGATTGAA-----GCG	318
Cy	422	aaggtacacacgcctttaccatgtgcacatgcacaaatgggtcgaagttcgaagttccat	481
Dc	319	AAGTATACACACGCTTTTACCATGGCAATGCACAAAGATCGAAGTTCCAAGTTC---	376
Cy	482	tgtctgagtgaggagaagaactactttttgatataccacaaggatctccagaactaa	541
Dc	376	-----TGGGCAAAACTACTTATTTGATATCCCAAGAAATTCGCAAAACTTAA	426
Cy	542	gtctcggattaagtttttggtagaagtgttgatataataatggcaattacttctc	601
Dc	427	GTTCCAGAT-----ATGGATTTGGGTATTTATTAACATTTGGCAATATTACTC	471
Cy	602	tgtctctggaaacctggcataggttcatctatgtctggtactctctgtataccaattca	661
Dc	472	TGTTCTTGGAAACCTGGCATATGTT-----GTACTTTTATACCAATTTCACA	517
Cy	662	actgttttactgtatgagaggtcttgatcatgcacatataatttggaaacagttgt	721
Dc	518	ACTGTTTACTGTGTATGAGGCGCTTGGATCTTGCAAT-----ACAGTGTGT	563
Cy	722	tgattacataaaggtctgatagacaataatagatgacagattccctatlttgacaataa	781
Dc	564	TGATTACATCAAGGCTGATGACAAATATAGATGCAGATTTCCCTATTTTG-----	616
Cy	782	ggagcagtgaggcatcagactataaagaattctatattgtgttaatggatcatcaga	841
Dc	616	-----GAGGCATCAGACTATAAAGATTTCTATTTGTGTATATGATCATCAGAGA	667
Cy	842	acaagcctgaataatacaaggaatacatccagtttatttactttcagctccaataata	901
Dc	668	ACAAGCCT-----ATCAATATCCAGTATATTCCTTTCACCTTCAAAATATA	714
Cy	902	gttaacctttgcgcgcagtcggttgaataatcttacttttaccgcggagagttcatgt	961
Dc	715	GTTAAACCTTTGCCGCAGTC-----TATCTTACTTTTACCGGAGAGTTCACTGT	765
Cy	962	gaattaaagcttgaatgagcatcaccttgttttagcggtgacactatccagcaaggtgt	1021
Dc	766	GAAATATPACGTAATGGGCAATACCTTTG-----GACCTATATCCAGCAAGGTGT	816
Cy	1022	tttgattatgaatttgagatcagaagaagtatactaccggaagcatgaggaattttgg	1081
Dc	817	TTTTATATTAATAATTGAGATCAGAGAGATGATATCTAC-----TTGG	859
Cy	1082	tgaatgtcagtttgaataatgaacataacacttgaacacacaaatgaacccgaataa	1141
Dc	860	TGATATCTACAGTTGAAAAAGAAACATACCTTGAAAAACATCAATGAACCCGA----	916
Cy	1142	ttagagtttttagtagcaattatgctttgttagtaagaagaagatgaatatattgtcca	1201
Dc	916	-----CAATATCTTTTGTATGAAGAAGCAAGTAAGTAATTTATGTCTCA	960
Cy	1202	gttgagagaatttggggcaagaagatcaagtatgtgtgtgtgagtgatataacaatgtcgggaag	1261
Dc	961	GATATCGGAATTTTG-----AGTGAGTGGAGTATATTAACAAATGTCTGGGAG	1006



QY 1262 gtgaagaccatcgaagaacacttgcctagatcgtgacgttctcgtaccatttg 1321  
 |||||  
 DB 1007 GTGAGACCATATGAGAAACCTTGGCTA-----CGTTTCGGCTACCATTTGG 1055  
 QY 1322 ttccatcttaattagttatatttgtaaccggtcgccttaagtgtgcgaagca 1381  
 |||||  
 DB 1056 TTTCATCTTATATTAATTAATTTGTAACCGGTGCTGCTT-----TTGCGTAACCCA 1107  
 QY 1382 aacacctaccacaaatgatccgaattttctgtatcatgaaga 1429  
 |||||  
 DB 1108 AACACTACCAAAATGATCCAGAAATTTTCTGTATCATGAGAA 1155  
 RESULT 9  
 T96784 standard: cDNA: 1126 BP.  
 AC T96784;  
 DT 30-MAR-1998 (first entry)  
 DE Celebus macaque Zcytor2 cDNA.  
 KW cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 OS Macaque sp. infertility; antagonist; contraceptive; diagnostic; therapeutic; ds.  
 FH Key location/Qualifiers  
 FT CDS 11..1126  
 FT /tag- a  
 FT /product- Zcytor2  
 FT /note- "cytokine receptor"  
 PN MO973913-11.  
 PD 18-SEP-1997  
 PR 12-MAR-1997; U04043.  
 PR 13-MAR-1996; US-013345.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ,  
 PI Ohara PJ;  
 DR MPI: 97-470820/43.  
 DR P-PSDB; W36616.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Example 4; Page 53-56; 79pp: English.  
 CS This cDNA sequence encodes a novel ligand-binding receptor, Zcytor2,  
 CC which shares homology with cytokine receptors and is isolated from  
 CC testis tissue obtained from a Celebus macaque. The resulting polypeptide  
 CC is a receptor for cytokines (particularly interleukin-13) and is  
 CC expressed on the surface of testicular cells, probably being involved in  
 CC spermatogenesis. It can be used to detect ligands promoting proliferation  
 CC and/or differentiation of such cells in cultures and may also be used to  
 CC treat infertility. Antagonists of this receptor may be used to  
 CC characterise ligand-receptor interactions and as male-specific  
 CC contraceptives. By blocking the action of IL-13, receptor antagonists and  
 CC ligand-binding this receptor can also be used to modulate immune  
 CC function, e.g. in allergy and asthma, as a diagnostic to determine  
 CC circulating levels of ligand and also to isolate and purify ligands.  
 CC Antbodies can be used to assay circulating receptor (an abnormal level  
 CC may be indicative of disease such as cancer), for labelling cells that  
 CC express the receptor, and therapeutically as antagonist.  
 CC Sequence 1126 BP; 359 A; 191 C; 227 G; 349 T;  
 SQ

Query Match 40.5%; Score 624; DB 1; Length 1126;  
 Best Local Similarity 79.3%; Pred. No. 1,2e-160;  
 Matches 1075; Conservative 0; Mismatches 50; Indels 231; Gaps 19;

DB 107 AACCCACCTCAGATTTTGAATAGTGAAT-----CCCGATATTTAGTTATAC 155  
 QY 224 tctatttgaaatggaaccccccacgtctctgatcatatttctgtgtgaaggaatga 283  
 DB 156 TCTATTTGCATGACAAACCCCACTCTCTGTGATATTTT-----AAGGAATGA 206  
 QY 284 cagtggaataatgaactaaataacccaacattggtagtgaaacatggaagcgtagttag 343  
 DB 207 CAGTGAATATGTAACAAATAATACCGAAACATTTGTTGTAACATGAGAG----- 257  
 QY 344 aggtaccatcattactaagaatctacattacaagaatggtgttgatcttaacagggca 403  
 DB 257 -----ACCATCATTTACTAAGAAATCTACATTAACAAATGGTTGATCTTAACAAAGGCA 311  
 QY 404 ttgaattatagaaggcgaagaatcacacgcctttaccatggcaatgacaaatgataca 463  
 DB 312 TTGAA-----GCGAAGATACACACACTTTTCCATGGCAATGCCAATGATGATCA 361  
 QY 464 gaattcacaagtccattgctagtagtggtggagaacactactatttgatcacacaca 523  
 DB 362 GAAGTTCAAAAGTTCC-----TGCGCAGAAGCTACTTATGATATCGCCACAAA 409  
 QY 524 ggaattccagaacactaaagttcaaggttaagtttgggtagaatgattgctatattac 583  
 DB 410 GGAATTCGAGAAACTAAAGTTCAAGAT-----ATGATGTTGTATATATTAC 454  
 QY 584 aattggcaatattactcctctcttggaacctgacatagttacattatgctgggtac 643  
 DB 455 AATTGGCAATATTACTCTGTCTTGGAACCTGGATAGGT-----GTAC 500  
 QY 644 ttcttgataccaattcaacttgcttactggtatgatatgaagccttgatcatgaataata 703  
 DB 501 TTCTATATACCAATTCACACTTGTTTACTGATAGAGGGCTGGATCGTCGATTT----- 556  
 QY 704 tatttggaacagtggtgtgattactatcaagcgtcatgtaacaaatatagttgcgaatt 763  
 DB 556 -----ACAGTGTGTTGATTACTATCAAGGTGTGAGCAAAATATTGATGACGATT 606  
 QY 764 tcccatattggcaataaagaagcaggaagcaccacataaagaattctatattgtg 823  
 DB 607 TCCCATTTTG-----GACTCATACAGCATATAAAGTTCTCATATTGGG 650  
 QY 824 ttaatgatacatcagaagaacagcctgaaataatcaagaatagatccagatttact 883  
 DB 651 TTAATGATCATCAGAAACCAAGCCT-----ATCAGATCCAGTATTACT 697  
 QY 884 ttcaacttcaaatatagtttaaaccttgcgcgcagtcagttgtaaatatttacttt 943  
 DB 698 TTTCACCTTCAAAATATTAATTAACCTTTGCCACCAAGTC-----TGCTTACTTGT 748  
 QY 944 actcgggaagttcaatgtaataatgaactgaatgaagacataccttggtagcggtga 1003  
 DB 749 ACTCAGAGAGATTATATTAATTAAGCTGAATGAGATACCTTTG-----GGA 799  
 QY 1004 cctattccagcaagtggtttgattatgaatggaattgagatcagaagaatgatactaccga 1063  
 DB 800 CCTATTCCAGCAAGGTGTTGTTGTTATGAATGAGATCAGAGAGATGATCTACAC--- 857  
 QY 1064 agcatggaaggaatttgggtgactgctacagttgtaaaatgaacatacacttgaagaaca 1123  
 DB 857 -----TTGGTGACTTACCCAGTTGAATAATGAACGTACACCTTGAATAATTA 902  
 QY 1124 caaatgaacccgaataatagagtttttagtagcaattatgcttggtagtaagaagcaaa 1183  
 DB 903 CAATATAAACCGA-----CACTTATGCTTTGTAGTAAAGAACAAA 943  
 QY 1184 gtgaatattattgtcagatgaacgaatttgggcaaaagaatcaagtaagtgtgagtg 1243  
 DB 944 GTGATATATTATTTGTCAGATGATGAATTTGG-----AGTAGTGAGAGTG 989  
 QY 1244 ataaagaatgctggggaaggtgaagacctatcgaagaacacttctgtagtagctggagatcg 1303  
 |||||



27-FEB-1997; AU-005374.  
 10-SEP-1996; AU-002262.  
 (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;  
 DR MPI: 98-207062/18.  
 DR P-RSD: W56261.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PT products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection  
 PS Disclosure: Page 19-20; 69pp; English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.  
 SO Sequence 947 BP; 312 A; 161 C; 198 G; 276 T;

Query Match 38.7%; Score 595; DB 1; Length 947;  
 Best Local Similarity 82.7%; Pred. No. 8.7e-153;  
 Matches 942; Conservative 0; Mismatches 0; Indels 197; Gaps 15;

QY 152 gagataaagtaaacctccctccagatttgaagatgtgattgaagaaccggat 211  
 DB 1 GAGATAAAGTAACCTCCCTCAGGATTGTGAGATAGTGAT-----CCCGGAT 49  
 QY 212 actaaggtatctctatcttgaatgcaagccacccctctctgagatcttgtgtc 271  
 DB 50 ACTAGGTATCTCTATTTGCAATGCACCCCACTGCTCTGATCATTTT----- 103  
 QY 272 gaaaggaatgcacagtggaatbatgaactaaataacgcgaacattgtgagtaacatgga 331  
 DB 103 --AAGGATGCGACAGTGGAAATATGACTAAATACCGAAACATGTGATGGAACATGGA 160  
 QY 332 aggtagtgtagaggttacatcatctcttagaatctacattaaagaatgggtttgac 391  
 DB 161 AG-----ACCATCTATTCTAAGAACTTACATTCACAAAGATGGGTTTATC 205  
 QY 392 ttaacaaaggcatgaaattatagaaggcgagaatatacacacgctttaccatggcaatgc 451  
 DB 206 TTAACAAGGCGCATGAA-----GCGAAGATACACAGCGCTTTACCATGGCAATGC 225  
 QY 452 acaaatggatcagaagatcagaatcccaattctgtagagtgggcgagaactactattgg 511  
 DB 256 ACAAAATGGATCAGAAAGTCAAAAGTTCC-----TGGCGACAGAACTACTTATTGG 303  
 QY 512 atataccacaagaattccagaactaaagttcagattaagtttgggtagaatggat 571  
 DB 304 ATATCACCAACAGAAATTCAGAAACTAAAGTTCAAGAT-----ATGAT 348  
 QY 572 tgcgtatatacaatctggcaatttactctgttcttggaaacttgcataagttacatt 631  
 DB 349 TGGGTATATTACATTTGGCAATATTACTGTTCTTGGAAACCTGGCAATAGT----- 403  
 QY 632 atgtcggggaactcttgtaaccaataaactgtttacttgatggagggcttgatc 691  
 DB 403 -----GTACTCTTGATACCAATTTACAACTGTTTACTGCTGTGAGGGCTTGATC 454  
 QY 692 atgcataataatatttggaaacagtggttgatcacaaagcgatgaggaacaaatat 751  
 DB 455 ATGCATTT-----ACAGTGTGTGATTTACATCAAGCGTGAATGGACAAATAAT 500  
 QY 752 aggatgcagaattccctatttggcacaataaaggcagtgagcatcagactaaagatt 811  
 DB 501 AGGATGCAATTTCCCTATTGTG-----GAGGATCAGACTTAAAGAT 544  
 QY 812 tctatatgtgttgaatgatactcagagaacagctgaatatcaagaatcagatcc 871  
 DB 545 TCTATATTGTTGTTAATGATCATCAGAGAACAGCT-----ATCAGATCC 591  
 QY 872 agtatttcaactttcagctcaaaatagtaaaccttgcgcagtcagttggaa 931

DB 592 AGTATTACCTTTTCAGCTTCAAAATATGTTAAACCTTTGCCGACGTC----- 643  
 QY 932 tatctacttctactcggagagtcacatgtaaatgaactgaagagacatcttg 991  
 DB 643 TATCTACTTTTACTCGGGAGAGTTTCAATGCAATTAAGCTGAATGAGACATCTTTG 702  
 QY 992 tttaggggtagacctatccagcaaggtgtttgattatgaatgaatcagaagaat 1051  
 DB 703 -----GGACCTATTCAGCAGAGGTGTTGATTGATGAATTAAGATGAGAGAT 753  
 QY 1052 gatactaccgaagcagtgaggaatttggtagctctcagttggaatgaacatata 1111  
 DB 754 GATACCTACC-----TTGGTACTCTCTACAGTTGAAATGAAATACATACA 796  
 QY 1112 ccttgaacaacaatgaacccgaataatagatttttagtaacatattccttga 1171  
 DB 797 CCTGAAACACAAATGAACCCGA-----CAATATGCTTTGTA 837  
 QY 1172 gtaagaacgaatgaaatttatttgcctagatgacggaatttggcaagaatacagta 1231  
 DB 838 GTAGAGAGCAAAAGTGAATATTATGCTCAGATGACGGAATTTG-----A 883  
 QY 1232 gtgagtgagtgataacaatgctgggaagtggaagacctacgagaagaacttgcta 1290  
 DB 884 GTAGAGTGAATGAATAACATGCTGGAGAGTGAGACCTATCGAAGAAACTTTGCTA 942

# RESULT 12

ID V89756  
 AC V89756; 789756 standard; cDNA; 456 BP.  
 DE 15-FEB-1999 (first entry)  
 KW Human; secreted protein; expressed sequence tag; EST; hematopoiesis;  
 KW Lissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;  
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;  
 KW gene therapy; ss.  
 OS Homo sapiens.  
 PN WO9845436-A2.  
 PD 15-OCT-1998.  
 PF 10-APR-1998; U06955.  
 PR 10-APR-1997; U0-838821.  
 FA (GENM) GENETICS INST INC.  
 PI Agostino MJ, Jacobs K, Lavallite ER, McCoy JM, Merberg D,  
 PI Racie JA, Spaulding V, Treacy M;  
 DR MPI: 99-070077/06.  
 PT New polynucleotides encoding human secreted proteins - derived from  
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,  
 PT ovary, pituitary, retina and colon cDNA libraries.  
 PS Claim 1; Page 320; 618pp; English.  
 CC The present sequence represents a human expressed sequence tag (EST).  
 CC The polynucleotide, which is a secreted EST, and the encoded protein  
 CC are predicted to have useful biological activities which would make  
 CC them suitable for treating, preventing or ameliorating medical  
 CC conditions in humans and animals, although no supporting data is  
 CC given. Suggested activities include nutritional activity, immune  
 CC stimulating or suppressing activity, hematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic  
 CC activity, receptor/ligand activity, anti-inflammatory activity,  
 CC cadherin/tumour invasion suppressor activity, tumour inhibition  
 CC activity. The polynucleotide may also be useful for gene therapy.  
 SO Sequence 456 BP; 142 A; 93 C; 92 G; 129 T;

Query Match 18.6%; Score 287; DB 1; Length 456;  
 Best Local Similarity 85.6%; Pred. No. 4.8e-09;  
 Matches 429; Conservative 0; Mismatches 0; Indels 72; Gaps 7;  
 QY 22 aggaatatacaggtttaatctcggagaatgcttaattgcttgcgtatcgg 81  
 DB 21 AGGCAATATCAAGGTTTAATCTCGGAAATGCT---TTGGTTGCTTGCTATCGG 77



PT New nucleic acid encoding interleukin-13 receptor binding chain and  
 PT transformed cells - proteins, antibodies and inhibitors, for  
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
 PT and in diagnosis  
 PS Claim 1, Pages 28-30; 49pp; English.  
 CC The present sequence encodes the murine Interleukin-13 (IL-13) binding  
 CC chain of the Interleukin-13 receptor, designated IL-13bc. IL-13bc acts a  
 CC mediator of the known biological activities of IL-13. The present  
 CC sequence was isolated from the thymuses of 6-8 week old mice. Recombinant  
 CC IL-13bc proteins, and antibodies raised against them, are used to  
 CC inhibit the binding of IL-13 to its receptor. They are particularly used  
 CC to treat IFN-mediated conditions, e.g. allergy, asthma and immune complex  
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.  
 CC They are also used to treat immune deficiency (particularly in  
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage  
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  
 CC with such activity is combined with IL-13bc and the mixture applied,  
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor  
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect  
 CC expression of IL-13, its receptor or binding chain, and to raise specific  
 CC antibodies which may be useful for treating some tumours.  
 SQ Sequence 1525 BP; 505 A; 246 C; 327 G; 447 T;

Query Match 15.4%; Score 237.4; DB 1; Length 1525;  
 Best Local Similarity 63.9%; Pred. No. 2.5e-55;  
 Matches 681; Conservative 0; Mismatches 201; Indels 183; Gaps 14;

QY 152 gaataaagatgaacccctcctcagatttgagatgagatgaggaacccgagat 211  
 DB 322 GAATATAAATTAATCTCTCAGGATTTGAATATGAT-----CTGGAT 370  
 QY 212 actaagttatctctatctgcaatgcaacccacgtctcgtgcatcttctgtgt 271  
 DB 371 TACTGTGTTCTCTCTTCTTCATGGAACCTCTGTGTTAGAAATTT----- 424  
 QY 272 gaaaggaatgcagatgagatgaaataaatacgaacaaatggtgagtaaatgga 331  
 DB 424 -AAGGCTGTACACTGAAATATGAGTAAATACCAATGTTGATACGACAGCTGGA 481  
 QY 332 aggtctgtagagaggtgacatctactaagaatctactaactcaagaatggttgc 391  
 DB 482 AG-----ACATAATTAATCTAGAAATCTAATTTACAAAGATGGGTTGATC 526  
 QY 392 ttaacaaggcatgaaatataagaaggcgaagatacacacgcgttttaccatgcaatgc 451  
 DB 527 TTATAAAGCATTTGAA-----GGAAGATACGTACGATTTGTCTGAGAGCATGT 576  
 QY 452 acaatgagatcagaagttcaaatctcaatctgtagagtggtgagcaaatctattgg 511  
 DB 577 ACAATGATGATCAGAAAGTCAAAAGTCC-----ATGATAGAAAGCTTTATGGG 624  
 QY 512 ataccaccaagaagaatccagaactaaagtccaggaatgaagtttggtagaagat 571  
 DB 625 ATATCGATCAAGAAAGTTGGAACTAAATTCAGCA-----CATGAAG 669  
 QY 572 tgcgtatattacatggaataatacttctctgtcttgcgaacatggtcatagttacatc 631  
 DB 670 TGTATATATATATACGTGCGATATTGCTGTGCTTGAACCTGCGCA----- 719  
 QY 632 atgtctggtgaactcttgcataccaactgttttactgtgtagaggttgatc 651  
 DB 719 ---AGACAGTATATTCGATACCAACTATCACTGTTTCTGTATGAGAGGCTTGATC 775  
 QY 692 atgcatataatataattggaacagtggtgtgtagatcaagtcgtagaataat 751  
 DB 776 ATCCCTT-----ACAGTGTCTGATTAATCTCCAGATGATATAAATAATGT 821  
 QY 752 aggaatgcagatttccctattggaataaaggagcagtgagacatcagactataaagat 811  
 DB 822 TGGATGCAAACTGTCCAACTG-----GACTCATCGATGATATAAAGATT 865  
 QY 812 tctatatctgttgaatgagatcagagaacaagcctgaataatacaaggaatcagatcc 871

DB 866 TTTTATCTGCTGTATATGATCTTCAAAAGTTGAACCC-----ATCAGATCC 912  
 QY 872 agttattcactttcaggttcaaaatagttaaaccttgcgcagcagtcagttgaa 931  
 DB 913 AGCTATACAGTTTTCCTCACTTCAAAATATAGTTAAACCTTCCACACG-----AA 963  
 QY 932 tacttacttctactcggagagttcatgtgaataaagctgaatgagacatcttg 991  
 DB 964 TTCTCTCATATTAATGATGAGATTCATGATATAGAAATGAATGAGACACCT--- 1021  
 QY 992 tttaagcgtggaactctccagcaagtggtttgattatgaataatgagatcagaagat 1051  
 DB 1021 -----GGAGGAGCCCTTCCACCAAGTTTACCTATGAAGAAATGTGATCCGAGAGAC 1074  
 QY 1052 gatctaccgaaagcctgaggaatttggtagctcagctgtaaaatgaacataca 1111  
 DB 1075 GATATTTCC-----TGGGACTCTCCACAGACAAACGATATGAACT 1117  
 QY 1112 ccttgaacacacaaatgaacccgaataatagagttttagtagaataatgcttgyta 1171  
 DB 1118 TGAAGAGGAGACCAATGAAA-----GTGAAGACCTATGCTTTT 1158  
 QY 1172 gtaagaagcaagtgaaattattgctcagatgacggaattgg 1216  
 DB 1159 GTAAAGATGTAAAGTCAATATATATGTCAGATGATGATTTGG 1203

RESULT 15  
 V22697  
 ID V22697 standard; DNA; 473 BP.  
 AC V22697;  
 DE 24-SEP-1998 (first entry)  
 KW Interleukin-13 binding protein N-terminal region gene.  
 KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;  
 KW autoimmune disease; antibody; immunotherapy; ss.  
 OS Homo sapiens.  
 FH key  
 FT CDS Location/Qualifiers  
 FT 19..426  
 FT /\*tag= a  
 FT /product= "IL-13 binding protein Open Reading Frame 1"  
 FT /note= "No start codon, stop codons given within  
 sequence"  
 FT 41..472  
 FT /\*tag= b  
 FT /product= "IL-13 binding protein ORF 2"  
 FT /note= "No start codon, stop codons given within  
 sequence"  
 FT 3..473  
 FT /\*tag= c  
 FT /product= "IL-13 binding protein ORF 3"  
 FT /note= "No start codon, stop codons given within  
 sequence."  
 CDS  
 MO9810638-1.  
 PD 19-MAR-1998  
 PF 10-SEP-1997; AU0591.  
 PR 27-FEB-1997; AU-005374.  
 PY 10-SEP-1996; AU-002262.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;  
 DR WPI: 98-207062/18.  
 DR P-PDB: W56252, W56253, W56254.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PT products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection  
 PS Claim 10; Page 43; 65pp; English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.

SQ Sequence 473 BP; 134 A; 92 C; 114 G; 131 T;

Query Match 14.48; Score 221.6; DB 1; Length 473;  
 Best Local Similarity 80.58; Pred. No. 3.1e-51;  
 Matches 352; Conservative 0; Mismatches 35; Indels 50; Gaps 6;

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OY 2 gtgcctgcggcgaggagaggaaggaatcaaggcttcaatcgcggaagtgtctaa 61
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DB 76 gtgcctgcggcgaggagaggaatcaaggcttcaatcgcggaagtgtctaa 133
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OY 62 ttgcttgcctgcgagatcgatgcttatataccttcgtagaagcacacatttggctgt 121
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DB 133 ttgcttgcctgcgagatcgatgcttatataccttcgtagaagcacacatttggctgt 192
    |||||||

OY 122 acaagctttgcaactcaatcctcagaacagagataaaagttaacctcccaagatttt 181
    |||||||
DB 193 -----ACCTCATCTTCAGACACCGAGATMAAAAGTTAACCTCTCAGGATTTT 240
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OY 182 gagaatgagatatagaagagaaccccgataactaggttatctctatttggcaatggcaac 241
    |||||||
DB 241 gagaatgagatatagaagagaaccccgataactaggttatctctatttggcaatggcaac 289
    |||||||

OY 242 ccccaactgctctggaatcatttggctgtgaaagaatgcacagtggaatatagaactaa 301
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DB 290 ccccaactgctctggaatcatttggctgtgaaagaatgcacagtggaatatagaactaa 340
    |||||||

OY 302 aatacggaaaacattggtagtgaaacatggaagagctagtgtagaagttaccatcattacta 361
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DB 341 AATACCGAAACATGTGATGTAAGCAATGGGAAG-----GACCATCATTA 387
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OY 362 agaattcacattacaagaatgggttgatcttaacaaggagcatggaattatagaagggcg 421
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DB 388 AGAATCTACAT--TACAAAGGATGGGCTTGGATCMTTAAACAAGGGCATTTGAAGGCGA 445
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OY 422 aagatacacacgctttt 438
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DB 446 AGTTACACACGTTT 462
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Search completed: January 20, 2000, 06:16:48  
 Job time: 4119 sec

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C 24	42.8	2.8	827	69	CNS00E3	AL069854	Drosophila
C 25	42.8	2.8	1025	69	CNS01472	AL104216	Drosophila
C 26	42.6	2.8	1001	69	CNS01400	AL103554	Drosophila
C 27	42.4	2.8	1101	69	CNS00E06	AL069493	Drosophila
C 28	42.4	2.8	1101	69	CNS010CR	AL098805	Drosophila
C 29	41.8	2.7	1101	69	CNS00E51	AL069787	Drosophila
C 30	41.6	2.7	1029	69	CNS0017V	AL074642	Drosophila
C 31	41.4	2.7	1101	69	CNS000B1	AL065414	Drosophila
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C 33	41.1	2.7	1035	69	CNS00E25	AL097523	Drosophila
C 34	40.8	2.7	872	50	A0066816	A0066816	A0066816
C 35	40.4	2.6	1086	69	CNS00YXK	AL096962	Drosophila
C 36	40.4	2.6	1101	70	CNS017KT	AL108167	Drosophila
C 37	40.2	2.6	1008	69	CNS002YX	AL066448	Drosophila
C 38	40.2	2.6	1001	69	CNS007BE	AL066533	Drosophila
C 39	40.2	2.6	396	72	AO172313	AO172313	HS-3183_A
C 40	40.2	2.6	341	40	AA921043	AA921043	VY75h06_r
C 41	40.0	2.6	942	69	CNS00601	AL065607	Drosophila
C 42	40.0	2.6	817	69	CNS005NP	AL053906	Drosophila
C 43	40.0	2.6	1101	69	CNS00F16	AL070721	Drosophila
C 44	40.0	2.6	1200	70	CNS016CO	AL106578	Drosophila
C 45	39.6	2.6	439	44	A0044648	A0044648	A0044648

## ALIGNMENTS

RESULT 1  
 A1798934 676 bp mRNA EST 06-JUL-1999  
 LOCUS we94e04.x1 Soares\_NFL\_T.GBC\_S1 Homo sapiens cDNA clone  
 DEFINITION IMAGE:2348766.3, similar to SW:1132, HUMAN Q14627 INTERLEUKIN-13  
 RECEPTOR ALPHA-2 CHAIN PRECURSOR, mRNA sequence.  
 A1798934  
 NID g5364406  
 VERSION A1798934.1 GI:5364406  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 676)  
 NCBI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189012.

FEATURES  
 source  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1350  
 Email: Robert.Strausberg@nih.gov  
 This clone is available royalty-free through LINT; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -400P from Gibco  
 High quality sequence stop: 468.  
 Location/Qualifiers  
 1..676  
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 /db\_xref="taxon:9606"  
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 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NDH19W, testis NHT, and B-cell  
 NCI-CGAP-GB1) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 682632-687239.

Query Match 726408-728711, and 729096-731399, Subtraction by Bento  
 Soares and M. Fatima Bonaldo.  
 BASE COUNT 205 a 133 c 117 g 221 t  
 ORIGIN

Best Local Similarity 82.6%; Pred. No. 3,5e-92;  
 Matches 660; Conservative 0; Mismatches 13; Indels 126; Gaps 10;

QY	741	ggacaaataaagagcagattcccatcttgcaataaagagcagcagcagca	800
DB	676	ggacacacatattagatcagatttccctatttg	633
QY	801	cttaaaagattcctatttggttgatagatcatagaagaacgctgaatacaag	860
DB	632	ctatagagatattctatttggtaaatagatcatagagagagcagcagcagcag	583
QY	861	gaatcagatccagattatcctcctcagctcgaataatagtaaccttgcgcag	920
DB	583	-ATCAATCAGCTTATTCACCTGTCAGCTCAAAATATTAACCTTGGCCGACG	526
QY	921	tcagttggaattatcttacttctcctcggagagtcattgtaaatgaattgaa	980
DB	525	TC-----TATCTTACTTTTACTCGGAGCTCATGTGAATTAAGCTGAATGGA	475
QY	981	gcataccttgtttagcgctgagcattccagcaaggtgtttgattataaattga	1040
DB	474	GCATACCTTTTG-----GGACCTATTCCAGCAAGGTGTTGATTAATAATTAGA	424
QY	1041	tcagagaataatattctaccgaagaacatgaggaatttgctcctcagattgaaa	1100
DB	423	TCGAGAAATATATCCACC-----TTGCTGACGTGTCACGTGAGAA	381
QY	1101	tgaacataccacttgaacaacacacacacacacacacacacacacacacacac	1160
DB	380	TGAACATACCTTGAACAAACAAACAAACAAACCA-----CAAT	340
QY	1161	tatgtttgttgaagaagaagaagaatttatgtctcagatgaggaatttgagca	1220
DB	333	TATGCTTGTGTAGTAAGCAAGTGAATTTATTTCTCAGATGGCGAATTGG-----	283
QY	1221	agaatcaagtagtagtagtagtagtaacaagtctgtaggaagtgaggaacctcaga	1280
DB	283	-----AGTAGTGGAGTGTATTAACAATCTGGGAGGGAACCTATCGAAGAA	234
QY	1281	aactttagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagt	1340
DB	233	AACCTTGCTA-----CGTTCTGCGTACATTTGGTTTCAATCTTAATATTAGTT	185
QY	1341	ataattgaacccgctgcttagtagtagtagtagtagtagtagtagtagtagtagt	1400
DB	184	ATATTGTAAACGCTGCTGCTT-----TTGGTAAAGCAACCCCTTAACCAAAATGA	133
QY	1401	ttccaagaatttctcgtgatacagaagaatttcacatttccatcagaagaacatg	1460
DB	132	TTCCAGAAATTTTCTGTGATACATGAAGA-----CTTTCATATCAAGAACATG	83
QY	1461	glattgactaagaagtttcagtcagtcagtcagtcagtcagtcagtcagtcagtcag	1520
DB	82	GTAATGACTAACAGTTTCCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG	23
QY	1521	attttcttcggaatttg 1539	
DB	22	ATTTTATTAACCAATCTTG 4	

RESULT 2  
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 LOCUS qy19c05.x1 NCI-CGAP-BRN23 Homo sapiens cDNA clone IMAGE:2012456.3  
 DEFINITION similar to SW:1132, HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2  
 CHAIN PRECURSOR, mRNA sequence.







QY 1157 caattatgcttctgtaagaagaagaagatgatatatttgcacagatgaggaatttg 1216  
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 QY 1217 gcaaaagaatcaagtagtgaagtgatgaataacatgctggaaggtgaagaccatga 1276  
 Db 275 -----ACTGAGTGCAGTGAATAACAAATGCGGAGAGTGAAGACCTATGCA 230  
 QY 1277 agaaaacttctgtagtgcggatcgttctgctgacacatttggttcaattatatt 1336  
 Db 229 AGAAACTTTCCTA-----CGTTCTGGCTACCACTTTGTTTCTATCTTAATTT 181  
 QY 1337 agtataattctgaacccgctccttagtgaatgctggaagcaaacaccaccacaaa 1396  
 Db 180 ACTTAATTTGTAAACCGGTCTGCTT-----TTGCGTAACCCAAACCTACCCAAA 129  
 QY 1397 atgattccagaatttctgctgatacagaagaattgcatcttccataccaagaga 1456  
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 QY 1457 catgtattgactcaacagttctcagtcacatgacgaatgtaataatgagctcaa-aa 1515  
 Db 78 CATGTATGTAGCTCAACAGTTCTCCAGTCATGSCCAATGTTCAATATGAGTCTCAACTAA 19  
 QY 1516 actgaatttctctgca 1533  
 Db 18 NOTGAAATTTCTTTCGA 1

RESULT 7  
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 LOCUS Y099f10.F1 Soares infant brain INIB Homo sapiens cDNA clone  
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 R52795  
 R52795.1 GI:814697  
 NID 9814697  
 VERSION R52795.1 GI:814697  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 473)  
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B.,  
 Chissoe, S., Dietrich, N., Dubucque, T., Favello, A., Gish, W.,  
 Hawkins, M., Hultman, M., Kucaba, T., Lacey, M., Le, M., Le, N.,  
 Marais, E., Moore, B., Morris, M., Parsons, J., Plange, C., Rifkin, L.,  
 Rohlfing, T., Schellendberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
 Trevasakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,  
 and Marra, M.  
 TITLE Generation and analysis of 280,000 human expressed sequence tags  
 JOURNAL Genome Res. 6 (9), 807-828 (1996)  
 MEDLINE 97044478  
 COMMENT

CONTACT: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewartson.wustl.edu  
 Insert Size: 1454  
 High quality sequence stops: 372 Source: IMAGE Consortium, LNL.  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
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 High quality sequence stop: 372.  
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 SOURCE Location/Qualifiers  
 1. 473  
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 /db\_xref="GDB:414189"  
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/clone="IMAGE:41448"  
 /clone.lib="Soares infant brain INIB"  
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 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: whole brain; Vector: latmid BA; Site: 1: Not  
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 AACGTGAAGATTCGGCGCCGCGAATTTTCTTTTCTTTT 3'];  
 double-stranded cDNA was ligated to Hind III adaptors  
 (pharmacia), digested with Not I and directionally cloned  
 into the Not I and Hind III sites of the latmid BA vector.  
 Library went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 134 a 92 c 114 g 131 t 2 others  
 ORIGIN

Query Match 14.4%; Score 221.6; DB 22; Length 473;  
 Best Local Similarity: 80.5%; Pred. No. 3.7e-43;  
 Matches 352; Conservative 0; Mismatches 35; Indels 50; Gaps 6;  
 QY 2 gtcctctgcgagggagagagagatcaatcatcaggttttaattctcgaggaatgcttaa 61  
 Db 76 GTGCTGTGCGGGGGGAGAGAGCAATATCAAGGTTTAAATCTGGAGAAATGGCT--- 133  
 QY 62 ttgcttctgctgctatcgatgctgttataaccttctgataagcacacattgctgt 121  
 Db 133 TTGCTTGTGCTTGGCTATCGAGTGTATTAACCTTCTGTATAGACAACTTGGCTGT 192  
 QY 122 acaagcttctgactcattctcagacacagagataaaagttaacctctcagatttt 181  
 Db 193 -----ACTTCATCTTCAACACACGAGATAAAAGTTAACCTCCACAGATTTT 240  
 QY 182 ggagatagtgattatgaagaagaacccgatacttagtctatctctatcttcaaggaac 241  
 Db 241 GAGATAGTGAGT-----CCCGATACTAGGTATCTCTATTTCATAGGCAAC 289  
 QY 242 cccacgtctctgattatcttctgtgtgtaagaagaatgcacagtggaatgaactaa 301  
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 QY 302 aatacgaacattgtagtgaacacatggaagcttagtgaaggttatcatatcata 361  
 Db 341 AATACCGAAACATTTGATGAGTAACATGGAG-----GACCATATTACTA 387  
 QY 362 agatctacattcaaaagatgaggttgaatcttaacaggacattgaatagaagggc 421  
 Db 388 AGAATCTACATT--TACAAAGGATGGGTTTGATGATCTTAAACAGGGCATTAAGCGCA 445  
 QY 422 aagatcacacagcttt 438  
 Db 446 AGTTACACACAGGTTT 462

RESULT 8  
 AA298563 365 bp mRNA EST 18-APR-1997  
 LOCUS EST114178 HSCI172 cells I Homo sapiens cDNA 5' end similar to IL13  
 DEFINITION receptor (IL13R), mRNA sequence.  
 R52795  
 R52795.1 GI:1950896  
 NID 91950896  
 VERSION AA298563.1 GI:1950896  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 365)  
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,  
 Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,  
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C.,  
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fitchman, J.L., Geoghagen, N.S.,  
 Glodet, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,  
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,  
 Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,  
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R.,  
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,  
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,  
 Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,  
 He, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,  
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,  
 Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,  
 Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,  
 Fraser, C.M., and Venter, J.C.  
 Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL MEDLINE  
 COMMENT  
 On Sep 12, 1996 this sequence version replaced gi:1393411.  
 Other ESTs: TNC194124  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1. 365

FEATURES  
 source  
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 /cell\_line="HSC172 (16PDL)"  
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 /note="Organ: lung; Vector: pbluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
 BASE COUNT 106 a 66 c 69 g 123 t 1 others  
 ORIGIN

Query Match 13.5%; Score 208.4; DB 31; Length 365;  
 Best Local Similarity 82.0%; Pred. No. 5.3e-40;  
 Matches 342; Conservative 0; Mismatches 2; Indels 73; Gaps 6;  
 507 attgataaccacacagaatccagaactaagaattcagaatttaagtttggtagaa 566  
 1 ATTCGATATCCACAGAAATTCACAACTAAGTTCAAGAT-----A 45  
 567 tggattcgtatatacaaatcgaataatactctgtcttggaaacctggcagaagtt 626  
 46 TGGATTCCGATATACAAATTCGCAATATTACTCTGTTCTGGAAACCTGGCATAGGT- 105  
 627 acattatcgtcgtggtactctctgtatccaattacaactctgttactggtatagggt 686  
 105 -----GTACTCTTGATACCAATTACACTGTTTACTGATAGAGGCTT 151  
 687 ggaatcgtacataataatatttgaacacagtggtgtattacatcaaggcgtgagacaa 746  
 152 GGTTCAGTACAT-----ACAGTGTGTGATTACATCAAGGCTGATGGACAA 197  
 747 aatatagatgacgaattccctatttggcaataaaggagcgtgagcactaagctataa 806  
 198 AATATAGATGACAGATTCCCTATTG-----GAGCATCAGACTATAA 241  
 807 agattctatattgtcttaatgatatcagagaacaagcctgaatatcaagaatca 866  
 242 AGATTCTATTATTGTTGTTAATGATCATCAGAACACAGCCT-----ATCA 288

QW 837 gatcccttattactt-ccgttcaaatatagtaaaccttgcgcagtc 922  
 DB 289 GATCCCTATTATTACTTTCACACTTCAAAATATACTTAACCTTGCAGCAGTC 345

RESULT 9  
 PG761600 469 bp DNA GSS 27-JUL-1999  
 DEFINITION  
 US 3132 B1 B05 T7C CIR Approved Human Genomic Sperm Library D Homo  
 sapiens genomic clone Plate-3132 Col-9 Row-D, genomic survey  
 sequence.  
 ACCESSION  
 AF761600.1 GI:5627410  
 VERSION  
 AF761600.1  
 SOURCE  
 Human.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE  
 1 (bases 1 to 469)  
 Mendiras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Furlong, J.,  
 Shaker, R., Schmidt, S., Traicoff, R., and Hood, L.E.  
 Construction of a Characterized Clone Resource for Genomic  
 Sequencing  
 Unpublished (1998)

JOURNAL COMMENT  
 Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones may be purchased from Research Genetics (info@resgen.com).  
 BAC end Web Server: <http://www.htsc.washington.edu>  
 Plate: 3132 row: D column: 9  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 469.  
 Location/Qualifiers  
 1. 469

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 source  
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 /db\_xref="taxon:9606"  
 /clone\_lib="Plate-3132 Col-9 Row-D"  
 /clone\_lib="CIR Approved Human Genomic Sperm Library D"  
 /sex="male"  
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 BASE COUNT 149 a 78 c 84 g 150 t 8 others  
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Query Match 4.9%; Score 75; DB 89; Length 469;  
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1260 aggtgaagacatcgcagaagaacttgcgtagtagcggagtagcttctggtcacatt 1319  
 272 AGGTGAAGACCTATCGAAGAGACTTGTCTA-----CGTNTCTGGCTACCATTT 320  
 1320 ggtttccttaatatagttatatttgaacgggtcgttgaatgttcgtagc 1379  
 321 GGTTCATCAATTAATATAGTTAATAGTAAACGGGTCTGCTT-----TTGGTAGC 372  
 1380 caaacactaccacaaatgat 1401  
 373 CAACACCTACCCAAATAGT 394

RESULT 10  
 CNS00396/C 1101 bp DNA GSS 03-JUN-1999  
 LOCUS  
 DEFINITION  
 Drosophila melanogaster genome survey sequence TET3 end of BAC #



## ORGANISMS

## AUTHORS

0000

1

3

616 49

676 ta

736-24

TM 400

794 KRI

•

076 St...

1036 tgagatcagaqaatqatactacccaattcccaaatcttcttttt

1050 yaaaaatgaaa 1105

1000

BACN15A12 of Drosophila genome survey sequence T7 end of BAC

9302280Z  
AT106638:1  
BT-----

ORGANISM *Drosophila melanogaster*

Direct Submitter

collaboration with the European Drosophila Consortium.

Location/Qualifiers

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/organism="Drosophila melanogaster"

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/clone_lib="DrosBAC"
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STAIN

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est 0.2348; prod no 0.0074
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855 atcaaggaatcatgatccagtatttacttt+acaact+caccccccttatc

915

.....ADAWDDADDAK 1024



RESULT 12  
LOCUS A1547789  
DEFINITION A1547789 160 bp mRNA EST 22-MAR-1999  
UI-R-03-s4-h-02-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone  
UI-R-03-s3-h-02-0-UI.3, mRNA sequence.  
ACCESSION A1547789  
MID 94465277  
VERSION A1547789.1 GI:4465277  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 160)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (?), 791-805 (1996)  
MEDLINE 97044477  
COMMENT On Jun 5, 1998 this sequence version replaced gi:3187484.

**CONTACT:** Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel.: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares lab clone distribution: clones will be available through  
 Research Genetics ([www.resgen.com](http://www.resgen.com))  
 Seq primer: M13 Forward  
 Location/Qualifiers  
 1. 160

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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/clone_lib="UI-R-C3"
/dev_stage="adult"
/lay_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site-1: Not I. Site-2: Eco RI. The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2p,
UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of

```

3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C3) was constructed as follows: PCR-amplified cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6:791-806, 1996)." 5' c 34 c 26 g 50 t

Query Match	3.2%	Score 48.6;	DB 48;	Length 160;
Best Local Similarity	65.1%	Pred. No. 0.1;		
Matches: 114;	Conservative	0;	Mismatches	33;
			Indels	22;
			Gaps	2;

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Cy 805 aaagatttcataattgltgtaatgatcatcagagaacacgccggaatatcaaggaat 864
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Db 8 AAAGCTTTTATTTCGTGTTATGATCCACAAAGCTGAGCCT-----AT 54

```

Eg.    865 cgaaccagttatttcaactttcagctccaataatagttaaacctttgcggccagtcag    924  
         |||||    |    |||||    |||||    |||||    |||||    |||||    |||||  
Eb     55 caaatccagctacatggtttttcaccttccaaatatataattaaaccattgccaccag---- 111

Q7. 925 ttgaaataatcttacttttaccggaaggttcacgtgaattaagctgaatatg 979  
 111 1 1 11111 1111 11 111 111 1 1111111  
 D8 111 ----AAATCCCTCATATTACTGTGAGAACTCTATTGACATTCAAATGAATGCG 1600

RESULT	13
CNS016FP	
LOCUS	
DEFINITION	CNCJ16FP 1201 bp DNA GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN15KR18 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION	AL106687
IND	35623252
VERSION	AL106687.1
KEYWORDS	GSS.
SOURCE	fruit fly.

**ORIGINISM** Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscocornipha; Ephydriidae; Drosophilidae; Drosophila.  
1 (bases 1 to 1201)

GENOSCOPE.  
 DIRECT SUBMISSION  
 Submitted (23-JUL-1999)  
 BP 101 61000 EVRY cedex - FRANCE (E-mail :  
 secretef@genoscope.cns.fr)

COMMENTS

- Web : [www.genoscope.cns.it](http://www.genoscope.cns.it) )  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CPHH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

```

FEATURES
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    Location/Qualifiers
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        /plasmid="pBelosBAC1"
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        171 g
        357 t
        197 others

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Best Local Similarity 31.0%; Pred. No. 0.87;  
Matches 91; Conservative 81; Mismatches 117; Indels 5; Gaps 1;

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OY 1018 gtgttttgaattgaattgagatcagagaagatgatactaccgaaagcatgagggaatt 1077
      ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1089 KKKKGAKAGTAAAKAKKADADADADADADADADADADADADADADADADADADAD 1030
      ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1078 ttggtgactgctacagctgaagaatgaacatacaccttgaaacaacaatgaaccoga 1137
      ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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      ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 1138 ataatagagtttttagtagcaatttgctt----gtagtaagaagcaagtgatatt 1192
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Db 969 AAAAAAAAAAAAAAAAAAKADADADADADADADADADADADADADADADADADADAD 910
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OY 1193 tatgctcagatgacggaatttgaggcaagaatcgaagtagtgagtgagtaacaat 1252
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Db 909 AAKAKRAAAAKAKAKADADADADADADADADADADADADADADADADADADADDD 850
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OY 1253 gctgggaaggtgaagaccatcgaaagaaacttgctagtagctgggagtcgltt 1306
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Db 849 AKAARAAAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 796
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Search completed: January 20, 2000, 05:25:26  
Job time: 6339 sec

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GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2000, 20:00:50 ; Search time 34.07 Seconds  
(without alignments)  
296.858 Million cell updates/sec

Title: US-09-077-317-4  
Perfect score: 2324  
Sequence: 1 MEMPARLGLMALLLCAGGG.....QTRKETSVALLENKKAQ 427

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A\_Geneseq.36.\*

Word size: 0

Number of hits that pass the threshold: 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2324	100.0	427	1	W24973	Human interleukin-13
2	2309.5	99.4	426	1	W09822	Human interleukin-13
3	1708.5	75.5	426	1	W09821	Mouse interleukin-13
4	942	40.5	177	1	W58937	Homo sapiens adult
5	318	13.7	415	1	R22211	Sequence of interl
6	318	13.7	415	1	R22217	Sequence of interl
7	318	13.7	398	1	R22212	Sequence of interl
8	302	13.0	372	1	W36616	Celebus macaque 2c
9	296.5	12.8	421	1	R25064	Human IL-5 recepto
10	295.5	12.7	380	1	W35295	Human IL-13 bindin
11	295.5	12.7	380	1	W36613	Human zcytor2 cyto
12	295.5	12.7	380	1	W41502	Human cytokine/pep
13	295.5	12.7	380	1	W33603	Homo sapiens HR-1
14	295.5	12.7	380	1	W24972	Human interleukin-13
15	295.5	12.7	380	1	W41520	Human HR-1 recepto
16	294.5	12.7	380	1	W36614	Human zcytor2 cyto
17	294.5	12.7	420	1	W83842	Human interleukin-13
18	293.5	12.6	420	1	R22215	Sequence of human
19	288.5	12.4	420	1	R22219	Sequence of secret
20	287.5	12.4	383	1	W35294	Murine IL-13 bindi
21	284	12.2	359	1	W56260	Construct containi
22	284	12.2	315	1	W56261	Mature interleukin
23	282.5	12.2	396	1	R22216	Sequence of human
24	281	12.1	396	1	R22220	Sequence of secret
25	260	11.2	312	1	R22213	Sequence of interl
26	260	11.2	312	1	R22214	Sequence of interl
27	260	11.2	332	1	R22218	Sequence of interl
28	236	10.2	1026	1	R70121	IL5-R-GBP 130 fusi
29	234	10.1	313	1	W21856	Protein used in pr
30	229	9.9	335	1	R25063	Soluble human IL-5
31	229	9.9	335	1	R33699	Shil-5R-alpha. Deo
32	228	9.8	360	1	R10919	Human GM-CSF recep
33	205.5	8.8	369	1	R59094	Murine IL-2R gamma
34	202	8.7	347	1	R47149	IL-2 receptor gamm
35	202	8.7	369	1	R47148	IL-2 receptor gamm
36	180	7.7	425	1	W70962	Rat zcytor5 protei
37	178	7.7	482	1	W31646	Human cytokine rec
38	178	7.7	452	1	R47150	IL-2 receptor gamm
39	178	7.7	230	1	R47151	IL-2 receptor gamm

## ALIGNMENTS

Result No.	Score	Query Match	Length	DB	ID	Description
1	2324	100.0	427	1	W24973	Human interleukin-13
2	2309.5	99.4	426	1	W09822	Human interleukin-13
3	1708.5	75.5	426	1	W09821	Mouse interleukin-13
4	942	40.5	177	1	W58937	Homo sapiens adult
5	318	13.7	415	1	R22211	Sequence of interl
6	318	13.7	415	1	R22217	Sequence of interl
7	318	13.7	398	1	R22212	Sequence of interl
8	302	13.0	372	1	W36616	Celebus macaque 2c
9	296.5	12.8	421	1	R25064	Human IL-5 recepto
10	295.5	12.7	380	1	W35295	Human IL-13 bindin
11	295.5	12.7	380	1	W36613	Human zcytor2 cyto
12	295.5	12.7	380	1	W41502	Human cytokine/pep
13	295.5	12.7	380	1	W33603	Homo sapiens HR-1
14	295.5	12.7	380	1	W24972	Human interleukin-13
15	295.5	12.7	380	1	W41520	Human HR-1 recepto
16	294.5	12.7	380	1	W36614	Human zcytor2 cyto
17	294.5	12.7	420	1	W83842	Human interleukin-13
18	293.5	12.6	420	1	R22215	Sequence of human
19	288.5	12.4	420	1	R22219	Sequence of secret
20	287.5	12.4	383	1	W35294	Murine IL-13 bindi
21	284	12.2	359	1	W56260	Construct containi
22	284	12.2	315	1	W56261	Mature interleukin
23	282.5	12.2	396	1	R22216	Sequence of human
24	281	12.1	396	1	R22220	Sequence of secret
25	260	11.2	312	1	R22213	Sequence of interl
26	260	11.2	312	1	R22214	Sequence of interl
27	260	11.2	332	1	R22218	Sequence of interl
28	236	10.2	1026	1	R70121	IL5-R-GBP 130 fusi
29	234	10.1	313	1	W21856	Protein used in pr
30	229	9.9	335	1	R25063	Soluble human IL-5
31	229	9.9	335	1	R33699	Shil-5R-alpha. Deo
32	228	9.8	360	1	R10919	Human GM-CSF recep
33	205.5	8.8	369	1	R59094	Murine IL-2R gamma
34	202	8.7	347	1	R47149	IL-2 receptor gamm
35	202	8.7	369	1	R47148	IL-2 receptor gamm
36	180	7.7	425	1	W70962	Rat zcytor5 protei
37	178	7.7	482	1	W31646	Human cytokine rec
38	178	7.7	452	1	R47150	IL-2 receptor gamm
39	178	7.7	230	1	R47151	IL-2 receptor gamm

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|||||
Db 241 DDLVQWENPQNFISRCLEFEVEVNNQSOTETHNVFYQEAKECENPEFERVENTSCFMP 300
QY 301 GVLPTLTNTVIRKVTNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLLIVPIYAGAI 360
Db 301 GVLPTLTNTVIRKVTNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLLIVPIYAGAI 360
QY 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLLIE 420
Db 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLLIE 420
QY 421 NLKRSQ 427
Db 421 NLKRSQ 427

RESULT 2
W09822 standard: Protein: 426 AA.
ID W09822:
AC W09822:
DT 15-JUL-1997 (first entry)
DE Human interleukin-12 receptor alpha chain NR4.
KW NR4: haemoprotein receptor; interleukin-13 receptor; IL-13;
KW cytokine; allergy; asthma; therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..27
FT /label= Sig_peptide
FT protein 28..426
FT /label= Mat_protein
FT domain 28..118
FT /label= Extracellular domain
FT /note= "Ig-like domain"
FT modified_site 36
FT /label= N-glycosylation site
FT modified_site 104
FT /label= N-glycosylation_site
FT domain 119..342
FT /label= Haemoreceptor_receptor-domain
FT modified_site 137
FT /label= N-glycosylation site
FT region 326..330
FT /label= WSDMS_motif
FT domain 343..366
FT /label= Transmembrane_domain
FT domain 367..426
FT /label= Cytoplasmic_tail
PN W09715663-A1.
PD 01-MAY-1997.
PF 23-OCT-1996; A00668.
PR 23-OCT-1995; AU-006135.
PR 22-DEC-1995; AU-007276.
PR 09-SEP-1996; AU-002208.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Hilton DJ, Metcalf D, Nicola NA, Willson T, Zhang JG;
DR WPI: 97-259018/23.
DR N-PSDB: T66165.
PT DNA encoding animal haemopoietin receptor which interacts with
PT interleukin-13 - useful to treat asthma, allergy or condition
PT exacerbated by IGE production
PS Claim 5; Page 52-54; 93pp; English.
CC Novel mouse and human haemoprotein receptors (W09821 and W09822),
CC designated NR4, comprise the interleukin-13 (IL-13) receptor
CC alpha-chain. The human NR4 amino acid sequence was deduced from
CC a composite DNA sequence (T66165) derived from bone marrow cDNA
CC clones. Recombinant NR4, or fusion proteins including NR4, can
CC be produced in transformed host cells. The receptor molecules and
CC their components are useful in the development of a range of
CC agonists, antagonists, therapeutics and diagnostic reagents based
CC on ligand interaction with its receptor, esp. for the development
CC of cpts. capable of modulating the activity of IL-13 and related
CC cytokines such as interleukin-4 for the treatment of allergy, asthma
CC and other conditions relating to IGE.

```

```

SQ Sequence 426 AA:
Query Match 99.4%; Score 2309.5; DB 1; Length 426;
Fast Local Similarity 99.8%; Pred. No. 2.3e-209;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLGLMALLICAGGGGGGGAAPTEQPEVNLISYVENLCTIVITWNPPEGASS 60
Db 1 MEMPARLGLMALLICAGGGGGGGAAPTEQPEVNLISYVENLCTIVITWNPPEGASS 59
QY 61 NCSLMTFSHEDKODKKIAPETRSIEVPLNERICLOVSGSCSTNESEKSIYVEKICSP 120
Db 60 NCSLMTFSHEDKODKKIAPETRSIEVPLNERICLOVSGSCSTNESEKSIYVEKICSP 119
QY 121 PEGPESAVTELOCIMWNLISYKCSWLPGRNTSPDTNTLYTHWRSLEKHOCENIREG 180
Db 120 PEGPESAVTELOCIMWNLISYKCSWLPGRNTSPDTNTLYTHWRSLEKHOCENIREG 179
QY 181 QYFGCSFDLTKVKDSFEQHSVQIMVKNAGKIKPSFNIVPLSRVAPDPPIKNSFEHN 240
Db 180 QYFGCSFDLTKVKDSFEQHSVQIMVKNAGKIKPSFNIVPLSRVAPDPPIKNSFEHN 239
QY 241 DDLVQWENPQNFISRCLEFEVEVNNQSOTETHNVFYQEAKECENPEFERVENTSCFMP 300
Db 240 DDLVQWENPQNFISRCLEFEVEVNNQSOTETHNVFYQEAKECENPEFERVENTSCFMP 299
QY 301 GVLPTLTNTVIRKVTNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLLIVPIYAGAI 360
Db 300 GVLPTLTNTVIRKVTNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLLIVPIYAGAI 359
QY 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLLIE 420
Db 360 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLLIE 419
QY 421 NLKRSQ 427
Db 420 NLKRSQ 426

RESULT 3
W09821
ID W09821 standard: Protein: 426 AA.
AC W09821:
DT 15-JUL-1997 (first entry)
DE Mouse interleukin-12 receptor alpha chain NR4.
KW NR4: haemoprotein receptor; interleukin-13 receptor; IL-13;
KW cytokine; allergy; asthma; therapy.
OS Mus sp.
FH Key Location/Qualifiers
FT peptide 1..27
FT /label= Sig_peptide
FT protein 28..426
FT /label= Mat_protein
FT domain 28..118
FT /label= Extracellular domain
FT /note= "Ig-like domain"
FT modified_site 36
FT /label= N-glycosylation site
FT modified_site 104
FT /label= N-glycosylation_site
FT domain 119..342
FT /label= Haemoreceptor_receptor-domain
FT modified_site 137
FT /label= N-glycosylation site
FT region 326..330
FT /label= WSDMS_motif
FT domain 343..366
FT /label= Transmembrane_domain
FT domain 367..426
FT /label= Cytoplasmic_tail
FT misc_difference: 21
FT /note= "unidentified amino acid"

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FT misc\_difference 194 /note- "unidentified amino acid"  
 PN W09715663-A1.  
 PD 01-MAY-1997.  
 PR 23-OCT-1996; AU00668.  
 PR 23-OCT-1995; AU-006135.  
 PR 22-DEC-1995; AU-007276.  
 PR 09-SEP-1996; AU-002208.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Hillon DJ, Metcalf D, Nicola NA, Willson T, Zhang JS;  
 DR WPI; 97-259018/23.  
 DR N-PSDB; T66164.  
 PT DNA encoding animal haemopoietin receptor which interacts with  
 PT Interleukin-13 - useful to treat asthma, allergy or condition  
 PT exacerbated by IGE production  
 PS Claim 5; Page 48-50; 93pp; English.  
 CC Novel mouse and human haemopoietin receptors (W09821 and W09822),  
 CC designated NR4, comprise the interleukin-13 (IL-13) receptor  
 CC alpha-chain. The mouse NR4 amino acid sequence was deduced from  
 CC a composite DNA sequence (T66164) derived from genomic and cDNA  
 CC clones. Recombinant NR4, or fusion proteins including NR4, can  
 CC be produced in transformed host cells. The receptor molecules and  
 CC their components are useful in the development of a range of  
 CC agonists, antagonists, therapeutics and diagnostic reagents based  
 CC on ligand interaction with its receptor, esp. for the development  
 CC of cabs. capable of modulating the activity of IL-13 and related  
 CC cytokines such as interleukin-4 for the treatment of allergy, asthma  
 CC and other conditions relating to IGE.  
 SQ Sequence 426 AA;

Query Match 73.5%; Score 1708.5; DB 1; Length 426;  
 Best Local Similarity 74.9%; Pred. No. 8.9e-153;  
 Matches 319; Conservative 40; Mismatches 66; Indels 1; Gaps 1;

QY 1 MEMPARLGLWALLLCAGGGGGGGAAPETQPPVNLVSVENLCTIVMTNPPEGASS 60  
 DB 1 MARPALLGELLVLLMTATVAGVAAA-TEVQPVNTLSVENVLCITIMWSPPEGASP 59  
 QY 1 NCSLWYSHHGDKDKKIAPETRSIEVPLNERICLOVSGSCSNESKPSILVEKCSIP 120  
 DB 60 NCLTRYSHEDQDDKIAPEHREKELPDEKICLOVSGSCSNESKPSILVEKCSIP 119  
 QY 121 PEGDESAVTELOCIMHNLSTYMKCSMLPGRTSPDTNTLYTLYMRSLEKIQCNIFREG 180  
 DB 120 PEGDESAVTELOCIMHNLSTYMKCSMLPGRTSPDTNTLYTLYMRSLEKIQCNIFREG 179  
 QY 181 QYFGCSFDLTKVKSSEQHSVQIMVKNACKIRSFENIVPLTSRVKRPDPHINKLSFNH 240  
 DB 180 CHINCSFLTLVEPXPSEHNVQIMVKNACKIRPSCKIVSLTSYVKRDPHINKLILKN 239  
 QY 241 DDLYVQENPQNFISRCLEFYEVENNSQTEHNFVQVQACENPEPERNENTSCFVNP 300  
 DB 240 GALLVQKNPNQNFISRCLEFYEVENNSQTEHNFVQVQACENPEPERNENTSCFVNP 299  
 QY 301 GVLDPDLTNTVIRKTNKLCYEDDKLMSNMQSEMSIGKRNSTLYITMLLIVPIYAGAI 360  
 DB 300 GVLDAVYTVAVRYKTNKLCYEDDKLMSNMQSEMSIGKRNSTLYITMLLIVPIYAVAV 359  
 QY 361 IVLLLYLKRKLIIFFPIPDGKIFKEMFGQNDTLHWKRYDIYKQKEETDSVLLIE 420  
 DB 360 IILFYLRKRLIIFFPIPDGKIFKEMFGQNDTLHWKRYDIYKQKEETDSVLLIE 419  
 QY 421 NLKRAA 426  
 DB 420 NLKRAA 425

RESULT 4  
 W58987  
 ID W58987 standard; Protein; 177 AA.  
 AC W58987;  
 DT 11-SEP-1998 (first entry)

DE Homo sapiens adult placenta clone DA136-11 encoded protein.  
 KW adult; placenta; cDNA library; clone DA136-11; secreted protein  
 KW autoimmune disease; anti-inflammatory; immune; stimulation  
 KW suppression;  
 OS Homo sapiens;  
 PN W09814576-A2;  
 PR 09-APR-1998.  
 PR 03-OCT-1997; U18007.  
 PR 04-OCT-1996; US-726237.  
 PA (GEMV) GENETICS INST INC.  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,  
 FJ Racine LA, Spaulding V, Treacy W;  
 DR WPI; 98-240082/21.  
 DR N-PSDB; Y11622.  
 FT Nucleic acids encoding novel secreted proteins - useful as, e.g.  
 PT anti-inflammatory, immuno-stimulatory or suppressing agents  
 F3 Disclosure; Page 81-82; 110pp; English.  
 CC The sequence is that of a secreted protein encoded by  
 CC an isolated polynucleotide which may be of use in the  
 CC production of therapeutic compositions for treating or  
 CC ameliorating a medical condition in a mammal. Such compositions  
 CC may be used for, e.g. research purposes as markers for  
 CC tissues, molecular weight markers for gels, primers or probes, for  
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be  
 CC used as a cytokine for cell proliferation and differentiation activity,  
 CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal  
 CC infections, for autoimmune diseases such as multiple sclerosis or  
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue  
 CC growth, as an activator or inhibitor, or as a chemotactic or  
 CC chemokine, haemostatic and thrombocytic, receptor/ligand,  
 CC anti-inflammatory or tumour inhibitor agents.  
 SQ Sequence 177 AA;

Query Match 40.5%; Score 942; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-81;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 MVKNACKIRPSFNIPLTSRVKRPDPHINKLSFHNDDLYVQENPQNFISRCLEFYEVEV 264  
 DB 1 MVKNACKIRPSFNIPLTSRVKRPDPHINKLSFHNDDLYVQENPQNFISRCLEFYEVEV 60  
 QY 265 NNSQTEHNFVQVQACENPEPERNENTSCFVNPGLDPLTNTVIRKTNKLCYEDD 324  
 DB 61 NNSQTEHNFVQVQACENPEPERNENTSCFVNPGLDPLTNTVIRKTNKLCYEDD 120  
 QY 325 KLSNMQSEMSIGKRNSTLYITMLLIVPIYAGAIIVLLLYLKRKLIIFFPIPD 381  
 DB 121 KLSNMQSEMSIGKRNSTLYITMLLIVPIYAGAIIVLLLYLKRKLIIFFPIPD 177

RESULT 5  
 R2221  
 ID R2221 standard; Protein; 415 AA.  
 AC R2221;  
 DT 22-JUL-1992 (first entry)  
 DE Sequence of Interleukin 5 (IL-5) receptor with signal peptide.  
 KW Autoimmune disorder; therapy; eosinophilia.  
 OS Mouse.  
 PN EP-475746-A.  
 PR 18-MAR-1992.  
 PR 11-SEP-1991; 308309.  
 PR 11-SEP-1990; JP-240638.  
 PA (TAKA) TAKATSU K.  
 PI Takatsu K, Tomimaga A, Takagi S, Murata Y;  
 DR WPI; 92-050329/12.  
 PT Human and murine interleukin-5 receptor and DNA encoding them -  
 PT for treatment of auto-immune and eosinophilia conditions  
 PT involving IL-5.  
 PS Claim 7; Page 21-23; 65pp; English.  
 CC The inventors claim: an isolated cDNA sequence encoding murine  
 CC secretory interleukin-5 (IL-5) receptor, which is synthesised from  
 CC murine early B cell mRNA; an isolated murine (secretory) IL-5

CC receptor; an isolated cDNA sequence encoding human (secretory) IL-5  
CC receptor, which is synthesised from mRNA of human peripheral blood  
CC eosinophils; and an isolated human (secretory) IL-5 receptor. Also  
CC claimed are a COS monkey cell transfected with a recombinant vector  
CC contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a  
CC transmembrane region; and an expression vector.  
Sequence 415 AA;

Query Match	13.7%;	Score 318;	DB 1;	Length 415;
Best Local Similarity	23.9%;	Pred. No. 7.5e-22;		
Matches 97;	Conservative 74;	Mismatches 179;	Indels 56;	Gaps 14

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OY      33  PPVNTLSVSVENLTCTVITAMP--EGGASSNCSLWYFSHF--GDKKDKIAETRSIEVPL  90
Db      29  PPV-NTITKAGLQAVLLHMPNPDPQEDRHNDLEYHKINAPQDEYEDTKRTESKCYPL  87
OY      91  NERICLQVGSOCSTNESEKPSILVEKICISPEGDPESAVELQCIWNL-----  140
Db      88  HEGFAASVRIILKSSHITLLASSWSVAELKAPGSPGISTVNLCTGTHVSSHTLHPQ  147
OY     140  SYMCSMLPGKNTSPDNTYTLTYNHRSLKTHGECNIFRE--GOYFGCSDDLTKVADSSF  197
Db     148  VSLRRTMLVGGKADBEDPDQYFLYRFFGYLVE--KCOEKSRLALNRTACWPPRFINSKGF  205D
OY     198  EOHSGVQIWMKNACKIKSFNIIVELTSSVKRDPDRPHIKNTLSHNDLTVQWENPQN--PISR  256
Db     206  EQLAVHINGSSKRAAIKRFDPQJESPLAIDQVNPFRANTVETIESNSLTIQWEKPLSAPDHI  265D
OY     257  CLPFEVEVNNQSOTETHNVFYVQEAKECENPERFERNVENTSCPMVPGVLPDLTNTVIRIVKT  316
Db     266  CFNFEIKLYINKNG-----HIQKEKLANKRISKIDVSY-----SIQVNAAV  309D
OY     317  NKLCLEDDKLTSMNSQSEIGSKKRNSTLYTMTLIVPIYAGALIVLLLYKRIKII--  374D
Db     310  SSPRMPEGR--GGEWSOPRIYVGKERKS--LVEMHLLIYLP---TAACFVLLIFSLICRWCHLM  364D
OY     374  --IRPPIDPGRKIFKEMGGDNDTLHMKKDIYEKQTEKTSBYV  417
Db     365  TRLPVPAPAKRSNIKL-----PVYTEKESKSNFKIEVV  399

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RESULT	6
R22217	
ID	R22217 standard; Protein: 415 AA.
AC	R22217;
DT	22-JUL-1992 (first entry)
DE	Sequence of interleukin 5 receptor (IL-5R.8).
KW	Autoimmune disorder; therapy; eosinophilla.
OS	Homo sapiens.
FT	Key
FT	peptide
FT	location/Qualifiers
FT	1..17
FT	/label= signal
FN	EP-4/5746-A.
PD	18-MAR-1992.
PF	11-SEP-1991. 308309.
PR	11-SEP-1990. JP-240638.
PA	(TAKA/) TAKATSU K.
PI	Takatsu K, Tomioka A, Takagi S, Murata Y;
DR	WPI; 92-090329/12.
DR	N-PSDB; Q22976.
PT	Human and murine interleukin-5 receptor encoding them -
PT	for treatment of auto-immune and eosinophilla conditions
PT	involving IL-5
PS	Disclosure: Page 45; 65pp; English.
CC	The inventors claim: an isolated cDNA sequence encoding murine
CC	(secretory) interleukin-5 (IL-5) receptor, which is synthesised from
CC	murine early B cell mRNA; an isolated murine (secretory) IL-5
CC	receptor; an isolated cDNA sequence encoding human (secretory) IL-5
CC	receptor, which is synthesised from mRNA of human peripheral blood
CC	eosinophils; and an isolated human (secretory) IL-5 receptor. Also
CC	claimed are a COS monkey cell transfected with a recombinant vector
CC	conty. the DNA; secretory human IL-5 lacking a cytoplasmic and a

CC transmembrane region; and an expression vector.  
SQ Sequence 415 AA;

Query Match 13.7%; Score 318; DB 1; Length 415;  
Best Local Similarity 23.9%; Pred. NO. 7.5e-22;  
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

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QY 233 PPAVNLASVYENLCTVIMTWMP--PEGASSNKSLWYFSHF--GDKODKLIARETSRISIEVPL 90
Dh 29 PPV--NFIITAKGLQVLLHMDPNFDOQRHVDLEYHNKINAPQEDVEDYDKTESKCTPL 87
QY 91 NERICLOVGSOCSTNESEKPSIIVEKICISPEGGDPESAVTELOCIMHNL----- 140
Dh 88 HEGPAASVRIKLSKSHITTLASSWVSABELKAPGSPGCHSVNLCTHTVAVSSHLPYQ 147
QY 140 SYMKCSMLPGHNISPDOTNITLYYHNHSLKELHOCENIFRE--GOYEGCSFDLTIKYDSSF 137
Dh 148 VSLRCTMTLVGKDAEDPQOYFLYRFYGLTLE--KCOEYSRALNBNRTACWPPRFFINSKGF 205
QY 198 EOHVVOIAMDNDACKIKRSPFIYVLTSNVRDPRIKINLSFNHDDLTVQOMENQON--EISR 256
Dh 206 EQLVNHINGSKRAAIRPDPOLSEPLAIDOVNPRNATVEIESLSLTIQOMEPLSAPBDH 265
QY 257 CLFEEVEVNNQSOTENHNVFYVOEAKCENPEFEREVENSTCFMNPBGVLPDLNTVIRIKVT 316
Dh 266 CFENELKTIYNNKNG-----HIQKRLKLANNFISKIDVSYT-----SIQVNAAV 309
QY 317 NKLCYEDDKLMSNKSQEMSIGKKNKNSFLYITMLLIVYVAGALIVLLYLKRLKIT-- 374
Dh 310 SSPCRMRGCR--WGEISSOPILYGKERKS--LVEMHLIVLR---TAAFCVLLIISLJCRCVHLM 364
QY 374 --TRPPRIPDPGRIKEMFGQNDOTLMMKKYDIYERKOTKEEDTSVY 417
Dh 365 TRLEPPVAPARSKIKDL-----PVUTEYERKSNSTKIEVV 399

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RESULT 7  
R22212  
IB R22212 standard; Protein; 398 AA.  
AC R22212;  
DE 22-JUL-1992 (first entry)  
DE Sequence of interleukin 5 (IL-5) receptor mature protein.  
KW Autoimmune disorder; therapy; eosinophilia.  
OS Mouse.  
PN EP-4/5746-A.  
PD 18-MAR-1992.  
PE 11-SEP-1991; 308309.  
PR 11-SEP-1990; JP-240638.  
PI (TAKA/) TAKATSU K.;  
PI Takatsui K, Tomiura A, Takagi S, Murata Y;  
DR WPI: 92-090329/12.  
PT Human and murine interleukin-5 receptor and DNA encoding them -  
PI for treatment of auto-immune and eosinophilia conditions  
PI Involving IL-5  
PS Claim 8; Page 24-25; 65pp; English.  
CC The inventors claim: an isolated cDNA sequence encoding murine  
(secretory) interleukin-5 (IL-5) receptor, which is synthesized from  
CC murine early B cell mRNA; an isolated murine (secretory) IL-5  
CC receptor; an isolated cDNA sequence encoding human (secretory) IL-5  
CC receptor, which is synthesized from mRNA of human peripheral blood  
CC eosinophil; and an isolated human (secretory) IL-5 receptor. Also  
CC claimed are a COS monkey cell transfected with a recombinant vector  
CC contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a  
CC transmembrane region; and an expression vector.  
SQ Sequence 398 AA;

Query Match 13.7%; Score 318; DB 1; Length 398;  
 Test Local Similarity 23.9%; Pred. No. 7e-22;  
 Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;  
 33 PPVNLSTVENVLCTVITWNP-PEGASSNCSLMTFSHF-GDKQDKTAPETRRRIEYPL 90



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DB 12 PPV-NFTIKATGLAQLVLLHMPDPOBQORHVDLEHYHVKINAPDEKXDTRESKCVPL 70
OY 91 NERCLQVSGSCSTSESEKPSILVEKICSPREGPESAVTELOCIMHNL----- 140
DB 71 HEGFAASVRIKLKSSHTTLLASSWVAELKAPGSPGTSVTLCTTHVSSSHLRLPYQ 130
OY 140 SYMCSMLPGNTSPDNTYTLWYHRSLEKIHOCENIFRE--GGYFGCSFDLTAKVDSF 197
DB 131 VSLRCLTDLVKGADPDQYFLYIRFGVLT--KQOYSRDLNNTACMPRTINSNGF 188
OY 198 EOHVSQIWMYDNACKIKRSPNIVPLTSRKPPPHIKNLSEHNDLYVOMENPON-FLSR 256
DB 189 EQLVHINGSKRAIKRPFQDLFSPPLADQVNPRTNVTIESNSLYQWEKPLSAFDPH 248
OY 257 CLFEVEVNSQTFTHNVFYQEAKECPENFEERNVENTSCMVGCVLPDLTNTVIRYKT 316
DB 249 CFNELKLYNTRKNG-----HLOKEKLLANKRISKIDVSTY-----SIOVRAV 292
OY 317 NKLCEYEDDKLMSNMSOESIGKRNSTLYITMLIVPIYVAGAILVLLYLKRLKII--- 374
DB 293 SSSPBMGR-WGMSQPIYVKEKRS-LVEWHLIVLP---TACFVLLIFSLICRVCHLM 347
OY 374 --TFPIPDGKIFKFNFGDNDTLHWKRYDIYKQTEEDSVV 417
DB 348 TRLEPVPAPKSNIKDL-----PVTEYKPSNETKIEVV 382

RESULT 8
ID W36616
AC W36616
DT 30-MAR-1998 (first entry)
DE Celebus macaque Zcytor2 protein.
KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
OS Macaque sp.
FH Key Location/Qualifiers
FT 1..372
FT /label=Zcytor2
FT /note="partial protein sequence"
PN W09733913-A1.
PD 18-SEP-1997.
PE 12-MAR-1997: U04043.
PR 13-MAR-1996: US-013345.
PA (ZYMO) ZYMOGENETICS INC.
PI Baumgartner JM, Farrah TM, Foster DC, Grant FU,
PI Ohara PJ.
DR N-PSDB: T96784.
DR WPI: 97-470820/43.
PT New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
PS Example 4: Page 56-57; 79pp; English.
CC This sequence represents a novel ligand-binding receptor, Zcytor2,
CC which shares homology with cytokine receptors and is isolated from
CC testis tissue obtained from a Celebus macaque. The resulting polypeptide
CC is a receptor for cytokines (particularly interleukin-13) and is
CC expressed on the surface of testicular cells, probably being involved in
CC spermatogenesis. It can be used to detect ligands promoting proliferation
CC and/or differentiation of such cells in cultures and may also be used to
CC treat infertility. Antagonists of this receptor may be used to
CC characterise ligand-receptor interactions and as male-specific
CC contraceptives. By blocking the action of IL-13, receptor antagonists and
CC ligand-binding this receptor can also be used to modulate immune
CC function, e.g. in allergy and asthma, as a diagnostic to determine
CC circulating levels of ligand and also to isolate and purify ligands.
CC Antibodies can be used to assay circulating receptor (an abnormal level
CC may be indicative of disease such as cancer), for labelling cells that
CC express the receptor, and therapeutically as antagonist.
CC Sequence 372 AA;

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Query Match 13.0%; Score 302; DB 1; Length 372;
Best Local Similarity 27.5%; Pred. No. 2e-20;
Matches: 95; Conservative 60; Mismatches 127; Indels 64; Gaps 19;

OY 52 WNPPEGAS--NCSLWTFSEFGDKKIAPEYRRST-----EVLNERICLVGS 100
DB 53 WQPLSLDNKEKTEVEY-----ELKYNISSEETWITITRNHLKDKGFDKIGKIAHIT 107
OY 101 -----QCSNTESEKPSILVEK--ISPEGPESAVTELOCIMHNLMSYKMSWLPGRNTSP 154
DB 108 LIPWQC--TNSSEVSSVAELTWTIS--PQILPEIKVQDMDCVYIMQYLCSMKPGISVLL 165
OY 155 DTNTTLYWHSLEKIHOCENIFRE--EGYFGCSFDLTAKVDSSEHQSVOIMYKDNAGKI 213
DB 166 DTNNLFTWYEGDLRALQCDYIKVDQNGICRPPY--LESSDVKDYICVNSSEETKPI 223
OY 214 KPSENIYPLTSRKVPDPPIKNSLSEHNDLY--VOMENPONFI-SCLTYEVEVNSQT 269
DB 224 RSSYFTPOLQNIYKPLPPVC--LTCIOESLYEIKLMSIFLGPAPCFYEIEIRDDYT 281
OY 270 ETHNVFYQEAKECPENFEERNVENTS--CFMVPGLPDLTNTVIRIRVKTNKLCEYEDDKL 326
DB 282 T-----LVTTVENETITLKITNETRQLCFVY-----RSKVNITC-SDDG1 321
OY 327 WSNRQIM--SIGKRNSTLYITMLIVPIYVAGAILVLLYLKRL 370
DB 322 WSEMSDKQCMVEBELKLTLL--LFLLP---GFIILIVFTGL 361

RESULT 9
ID R25064
AC R25064
DT 10-DEC-1992 (first entry)
DE Human IL-5 receptor alpha chain.
KW Interleukin-5; chronic asthma; eosinophilia;
KW screening antagonists; ss.
OS Homo sapiens.
PN EP-492214-5.
PU 01-JUL-1992.
PE 06-DEC-1991: 120951.
PR 27-DEC-1990: EP-811030.
PR 30-APR-1991: EP-810327.
PA (HOEF) HOFEMANN IA ROCHE & CO AG F.
PI Devos R, Fiers W, Plaetnick G, Tavernier J, Van Der Hayden J,
DR WPI: 32-218502/27.
DR N-PSDB: Q25790.
PT Recombinant alpha chain of human interleukin-5 receptor - and DNA
PT encoding it, for treatment of interleukin-5 mediated disorders
PT such as chronic asthma
PS Claim 7; Fig 1; 15pp; English.
CC This amino acid sequence was deduced from the nucleotide sequence,
CC isolated as detailed in Q25790. The cytoplasmic domain is 58 amino
CC acids long. A domain implicated in signal transduction processes
CC can not be found in this short cytoplasmic tail. Recombinant IL-5
CC alpha chain can be used as an IL-5 antagonist in chronic asthma or
CC other disease states with demonstrated eosinophilia. It may also be
CC used either alone or with the beta chain of the whole IL-5 receptor
CC as a tool for screening for IL-5 antagonists. See also Q25790-2, R25063.
CC Sequence 421 AA;

Query Match 12.8%; Score 296.5; DB 1; Length 421;
Best Local Similarity 24.8%; Pred. No. 8.1e-20;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

OY 33 PVTNLSVSENCTVITWNP--PEGASSNCSLWTFSEFGDKKIAPEYRRSIEVPLN 91
DB 32 PPV-NFTIKATGLAQLVLLHMPDPOBQORHVDLEHYHVKINAPDEKXDTRESKCVPL 70
OY 92 ERICLOV-----GSQCSNTESEKPSILVEKICSPREGPESAVTELOCIMHNL--- 140
DB 83 ESKCVTILTKGFSASVRIILQNDHSHLASSWVAELKAPGSPGTSVTLCTTHVSSSHLRLPYQ 130

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QY 140 -----SY-----MKCSWLPGRNTSPDTNLTLYWHRSLKIHQCNENIFR--GOYFGCSFDL 189  
 DB 143 YSRLRSTQVSLHCTWLVGIDAPEDTQYFLYKRGSWTE--ECQESKDITGRINIACFR 200  
 QY 190 TKVKSSFEQHSVOIMVKDNAGIKRSENIIVPLTSRYKPPPHIKNISFHNDDLYOWEN 249  
 DB 201 TFLISGRDMLSVLVNGSSKHSARPDQLFALHAIQINPPLNVAIEIGTSLISOMER 260  
 QY 250 POF-FISRCLEFEVENNSQTEETHNFFYQEAECNEFEERNENNTSCENAVPCLPTLN 308  
 DB 261 PVSAPFPHCDYEVKTHNTNG-----YDQIEKLTNAFISIIDDSKY----- 305  
 QY 309 TVRIRVTKNLCEYEDKLSMWSQEMSGIKRRNSTLYITMLIVPVAGAIIVLLYK 368  
 DB 305 DVGVRVAVSSMCREAG-LMSEWSQPIYGVNDEKHPLEMEVVIYIMATICFILLISLICK 363  
 QY 369 --RLKIIIPPIPDGKIFKEMFGDONDTLHMKKIDYIKQTKRETSVYL 418  
 DB 364 ICHLMWIKLPPIAPKSNIKDLFVTN-----YKAGSSSETEIEVI 404

RESULT 10  
 W35295  
 ID W35295 standard; Protein: 380 AA.  
 AC W35295;  
 DT 27-MAR-1998 (first entry)  
 DE Human IL-13 binding chain of the IL-13 receptor.  
 KW Interleukin-13; IL-13; Interleukin-13 receptor binding chain; IL-13bc;  
 KM mediator; IL-13 receptor binding inhibition; IgE-mediated condition;  
 OS allergy; asthma; immune complex disorder.  
 OS Homo sapiens.  
 FT Peptide  
 FT 1. 25  
 FT /label= signal\_sequence  
 FT /note= "putative"  
 FT 26. 380  
 FT /label= mature\_protein  
 FT 26. 341  
 FT /label= extracellular\_domain  
 FT 342. 362  
 FT /label= transmembrane\_domain  
 FT 363. 380  
 FT /label= intracellular\_domain

MO9731946-A1.  
 PD 04-SEP-1997.  
 PE 28-FEB-1997; U03124.  
 PR 01-MAR-1996; US-609572.  
 PA (GENE) GENETICS INST INC.  
 PI Collins M, Donaldson D, Filz L, Neben T, Whiters M,  
 PI Wood C;  
 PI WPI: 97-448632/41.  
 DR N-PSDB: T95214.  
 PT New nucleic acid encoding interleukin-13 receptor binding chain and  
 PT transformed cells - proteins, antibodies and inhibitors, for  
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
 PT and in diagnosis  
 PS Claim 11: Pages 34-35; 49pp; English.  
 CC The present sequence represents the human interleukin-13 (IL-13) binding  
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a  
 CC mediator of the known biological activities of IL-13. Recombinant  
 CC IL-13bc proteins, and antibodies raised against them, are used to  
 CC inhibit the binding of IL-13 to its receptor. They are particularly used  
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex  
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.  
 CC They are also used to treat immune deficiency (particularly in  
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage  
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  
 CC with such activity is combined with IL-13bc and the mixture applied,  
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor  
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect  
 CC expression of IL-13, its receptor or binding chain, and to raise specific  
 CC antibodies which may be useful for treating some tumours.

SQ Sequence 380 AA:  
 Query Match 12.7%; Score 295.5; DB 1: Length 380;  
 Best Local Similarity 26.0%; Pred. No. 8,6e-20;  
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 10 LNALILCAGGGGGGGAAPTEPTNTNSVENICTYIWMNPEGAS--SNCSLWTF 67  
 DB 11 LVFFLSTFTFGCGSSSDTEIKVNPQDFEIVDPGYGLYGLQWQPLSLDHRKECTVEV- 70  
 QY 68 SHEGKQDKKIAPETRRSI-----EVLNERICLOVGS---QCSNSEKPSILY 114  
 DB 70 ---ELKYNIGSEETKTIITNLHAKDGFIDNKGEAKIHTLLPQC-TNSESQSSWA 124  
 QY 115 EHC--ISPEGPDESAVTELOCIMHNLSTYMKCSWLPGRNTSPDTNLTLYWHRSLKIHQ 172  
 DB 125 ETTWTLS-PQGIPEIKVQMDCVYIMWOYLCSMKRPGISVLDNTINLTFTWEGDLHALQ 183  
 QY 173 C-ENIRREGQYEGCSFDLTKVDSFEQHSVOIMVKDNAGIKRSENIIVPLTSRYKPPDP 231  
 DB 184 CVDYIKADQGNIGCRPPYLEASD--YKDFYICVNGSSEKPIRSSYFTQLQNIYKPLPP 241  
 QY 232 HIKNLSFHNDD--DLVQENPQNTI--SRCLYEVEVANSQTEETHNFFYQEAECENPEF 287  
 DB 242 --VYLFRESSECEIKLKSIPDIPARCFDEIEIRDDYT-----LVATAVENERY 293  
 QY 288 ERNVENTS---CFMVGVLPTDLNTVIRIRVTKNLCEYEDKLSMWSQEM-----SIGK 339  
 DB 294 TLKTTTETHQLCFVV-----RSKVNITC-SDDGIWSENSDQCQEGEDLSK 339

QY 340 RNSTLYITMLIVPVAGAIIVLLYLKRLKIIIPPIPDGKIFKEMFGD 391  
 DB 340 TLRFPLPF-----GFILIVFVGL--LKRKPTTY-KMIPERFCD 379

RESULT 11  
 W35613  
 ID W35613 standard; Protein: 380 AA.  
 AC W35613;  
 DT 30-MAR-1998 (first entry)  
 DE Human Zcytor2 cytokine receptor protein.  
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.  
 OS Homo sapiens.  
 FT Key  
 FT Location/Qualifiers  
 FT Domain 340. 363  
 FT /label= transmembrane\_domain  
 FT Domain 364. 380  
 FT /label= intracellular\_domain  
 FT Domain 25. 339  
 FT /label= ligand\_binding\_domain

MO9733913-A1.  
 PD 18-SEP-1997.  
 PE 12-MAR-1997; U04043.  
 PR 13-MAR-1996; US-013345.  
 PA (ZYMO) ZYMOGENETICS INC.  
 PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ,  
 PI Ohara PJ;  
 PI WPI: 97-470820/43.  
 DR N-PSDB: T96782.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Claim 2: Page 47-48; 79pp; English.  
 CC This sequence represents a novel ligand-binding receptor. Zcytor2,  
 CC which shares homology with cytokine receptors and was isolated from human  
 CC placental polyA+ RNA. The resulting polypeptide is a receptor for  
 CC cytokines (particularly interleukin-13) and is expressed on the surface  
 CC of testicular cells, probably being involved in spermatogenesis. It can  
 CC be used to detect ligands that promote proliferation and/or  
 CC differentiation of such cells in cultures and may also be used to treat  
 CC infertility. Antagonists of this receptor may be used to characterise



PR 12-JUN-1996; US-017843.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI (SMIR) SMITHKLINE BEECHAM CORP.  
 DR Appelbaum ER, Hu J.  
 WI: 98-052309/05.  
 DR N-PSDB: V02295.  
 PT DNA encoding human cytokine-peptide hormone receptor - useful for  
 PT treating preventing or diagnosing, e.g. lowered resistance to  
 PT infection, asthma, allergy, or haematopoietic disease  
 PS Claim 15; Fig 1: 75pp; English.  
 CC The sequence is that of the human cytokine/peptide hormone receptor  
 CC (HR-1 receptor). This, or it's activators or agonists, can be used to  
 CC treat, prevent or diagnose predisposition to lowered resistance to  
 CC infection, asthma, allergic or haematopoietic disorders, e.g. where  
 CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,  
 CC neutropenia or cytotoxic treatments for cancer. Antagonists of the  
 CC receptor, e.g. antibodies or fragments of it may be used to treat  
 CC conditions associated with overexpression of the HR-1 receptor, e.g.  
 CC those listed above. Antibodies may also be used to assay levels of HR-1  
 CC receptor, overexpression of which may be diagnostic of tumours, by usual  
 CC immunoassays, to isolate and identify HR-1 receptor-expressing cells; or  
 CC for affinity purification of the HR-1 receptor.  
 SQ Sequence 380 AA;

Query Match 12.7%; Score 295.5; DB 1; Length 380;  
 Best Local Similarity 26.0%; Pred. No. 8.6e-20;  
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

OY 10 LMALLCAGGGGGGGAAPETOPPTNLVSVENLCTVITWNPPEGAS--SNCSLMYF 67  
 DB 11 LYTFLISTFCTSSSDTEIKVNPPOFEIVDPGLVLYQMPPLSLDHFECTVEY- 70  
 OY 68 SHFGDKODKRIAPETRSI-----EVLNERICLOVGS-----QCSNSESKEPSILV 114  
 DB 70 -----ELKRNIGSETWTTITITKLNHYDGDGLNKIGIAKIHILLPQC--TNGSEVOSSWA 124  
 OY 115 EKC--ISPPEGDSAVTELOCIMHNLVYKCSMLPGRNTPDNTNLYVHRSLEKIQ 172  
 DB 125 ETTVMIS--PGIPEETKVQDMDCVYNNQYLLCSMKRIGIVLDTNINLFETWIEGDLHALQ 183  
 OY 173 C-ENIFREGGYFGCSPLDTKVKSSFEQHSVQIMVKNAGKIKPSFNIVPLTSRYKPPDP 231  
 DB 184 CVDYIKADGONIGCRPPYLEASD--YKDEYICVNGSSEKPKRSSYFTFOLQNIYKPLP 241  
 OY 232 HINKLSFHDND--DLYVWENPQNF1-SRCLFEYEVNNSQETNHNVYVQAKCENPEF 287  
 DB 242 --VLLFTFRSSCEIKLMSIPLGPIPARCFYEIIRDDTT-----LVATVENEY 293  
 OY 288 ERNVENTS---CEMPGVLPDILNTVIRVKTNKLCEYEDDKLMSNMSQEM-----SIGRK 339  
 DB 294 TLKTTMETNQLCEVY-----RSKVNICY-SDDGIWSEMSDKQCEGEDLSKR 339  
 OY 340 RNSTLYITMLIVPVVAGAIIVLLYLKRLKIIIFPIPPGKIFKMGED 391  
 DB 340 TLLEFWLP-----GFIILVIVFTGL--LTKRPNTYF-KMIPFEFD 379

RESULT 14  
 ID W24972  
 AC W24972; standard; protein; 380 AA.  
 DT 22-JUN-1998 (first entry)  
 DE Human interleukin-13 beta receptor.  
 KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.  
 OS Homo sapiens.  
 PN W09720926-A1.  
 FD 12-JUN-1997.  
 PF 07-NOV-1996; F01756.  
 PR 06-DEC-1995; FR-014424.  
 PA (SNFI) SANOFI SA.  
 PI Caput D, Ferrara P, Laurent P, Vita N,  
 DR WPI: 97-319773/29.

DR N-PSDB: T85826, T86464.  
 PT New purified human interleukin-13 receptors - and related nucleic  
 PT acids, useful for diagnosis and treatment of inflammation, allergy,  
 PT etc.  
 PS Claim 1; Figure 2a; 83pp; French  
 CC This sequence represents interleukin-13 (IL-13) beta receptor. The  
 CC invention relates to new purified peptides comprising 380 or 427 amino  
 CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
 CC affinity, but acquires high affinity when associated with the IL-4  
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as  
 CC such as loss of heterozygosity and rearrangements, or chromosomal  
 CC anomalies. They are also used for production of recombinant IL-13R beta  
 CC and alpha which can be used as IL-13 antagonists, specifically to  
 CC regulate IL-13-induced responses for treatment of inflammation and  
 CC allergy (blocking synthesis of IL-13R). Antibodies are used (in standard  
 CC immunoassays) to diagnose diseases associated with abnormal expression  
 CC of IL-13 receptors; when coupled to a toxin also for treatment of  
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are  
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta  
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the  
 CC specification (T86464), which is not the same as that shown in the  
 CC sequence listing (T85826).  
 SQ Sequence 380 AA;

Query Match 12.7%; Score 295.5; DB 1; Length 380;  
 Best Local Similarity 26.0%; Pred. No. 8.6e-20;  
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

OY 10 LMALLCAGGGGGGGAAPETOPPTNLVSVENLCTVITWNPPEGAS--SNCSLMYF 67  
 DB 11 LYTFLISTFCTSSSDTEIKVNPPOFEIVDPGLVLYQMPPLSLDHFECTVEY- 70  
 OY 68 SHFGDKODKRIAPETRSI-----EVLNERICLOVGS-----QCSNSESKEPSILV 114  
 DB 70 -----ELKRNIGSETWTTITITKLNHYDGDGLNKIGIAKIHILLPQC--TNGSEVOSSWA 124  
 OY 115 EKC--ISPPEGDSAVTELOCIMHNLVYKCSMLPGRNTPDNTNLYVHRSLEKIQ 172  
 DB 125 ETTVMIS--PGIPEETKVQDMDCVYNNQYLLCSMKRIGIVLDTNINLFETWIEGDLHALQ 183  
 OY 173 C-ENIFREGGYFGCSPLDTKVKSSFEQHSVQIMVKNAGKIKPSFNIVPLTSRYKPPDP 231  
 DB 184 CVDYIKADGONIGCRPPYLEASD--YKDEYICVNGSSEKPKRSSYFTFOLQNIYKPLP 241  
 OY 232 HINKLSFHDND--DLYVWENPQNF1-SRCLFEYEVNNSQETNHNVYVQAKCENPEF 287  
 DB 242 --VLLFTFRSSCEIKLMSIPLGPIPARCFYEIIRDDTT-----LVATVENEY 293  
 OY 288 ERNVENTS---CEMPGVLPDILNTVIRVKTNKLCEYEDDKLMSNMSQEM-----SIGRK 339  
 DB 294 TLKTTMETNQLCEVY-----RSKVNICY-SDDGIWSEMSDKQCEGEDLSKR 339  
 OY 340 RNSTLYITMLIVPVVAGAIIVLLYLKRLKIIIFPIPPGKIFKMGED 391  
 DB 340 TLLEFWLP-----GFIILVIVFTGL--LTKRPNTYF-KMIPFEFD 379

RESULT 15  
 ID W41520  
 AC W41520; standard; protein; 380 AA.  
 DT 22-JUN-1998 (first entry)  
 DE Human HR-1 receptor.  
 KW HR-1 receptor; human; cytokine; infection; asthma; allergy;  
 KW haematopoietic disorder; tumour; therapy; diagnosis.  
 OS Homo sapiens.  
 FH Key  
 FT Peptide 1. 21  
 Location/Qualifiers

FT	Protein	/label= Sig_peptide
FT		22..380
PN		/label= Mat_protein
PD	MO9747741-A1.	
PD	18-DEC-1997.	
FF	12-JUN-1996; U10262.	
PR	12-JUN-1996; WO-U10262.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
PI	Appelbaum ER, Hu J:	
DR	WPI: 98-052308/05.	
DR	N-PSDS: V04131.	
PT	Nucleic acid sequence encoding human cytokine peptide hormone	
PT	receptor - useful to treat, prevent or diagnose, e.g. lowered	
PT	resistance to infection, asthma, allergy or haematopoietic disease	
PS	Claim 13: Page 62-64; 76pp; Eng11sh.	
CC	This protein comprises a novel human cytokine/peptide hormone	
CC	receptor, designated the HR-1 receptor, that shows 27% identity	
CC	and 52% similarity to the interleukin-5 receptor. Its amino acid	
CC	sequence was deduced from a cDNA clone (see V04131) obtained from a	
CC	human testis library. Recombinant HR-1 receptor can be expressed	
CC	in claimed host cells, and used in a claimed method for identifying	
CC	compounds which bind to, and activate or inhibit, it. HR-1	
CC	receptor activators and agonists can be used to treat, prevent or	
CC	diagnose predisposition to lowered resistance to infection, asthma,	
CC	allergic or haematopoietic disorders, e.g. where induced by AIDS,	
CC	aplastic anaemia, neutropenia or cytotoxic treatments for cancer.	
CC	HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can	
CC	be used to treat conditions associated with HR-1 receptor	
CC	overexpression. The antibodies can also be used to determine HR-1	
CC	receptor levels, since overexpression may be diagnostic of tumours.	
QO	Sequence 380 AA:	

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 19, 2000, 14:58:48 (Search time 71.05 seconds  
(without alignments)  
283.481 Million cell updates/sec

Title: US-09-077-817-4  
Perfect score: 2324  
Sequence: 1 MEMPARLGLMALLCAGCG.....QFKERTSVLLENKASQ 427

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database: PIR\_62.\*

Word size: 0

Number of hits that pass the threshold: 142080

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	13.7	415	2	SI2357
2	294.5	12.7	420	2	SI21052
3	283.5	12.2	356	2	SI21050
4	230	9.9	333	2	SI21053
5	229	9.9	335	2	SI21053
6	228	9.8	400	2	SI21053
7	207	8.9	373	2	SI21053
8	205.5	8.8	369	2	SI21053
9	202	8.7	369	2	SI21053
10	197.5	8.5	831	2	SI21053
11	190	8.2	610	2	SI21053
12	189	8.1	610	2	SI21053
13	189	8.1	412	2	SI21053
14	189	8.1	310	2	SI21053
15	186	8.0	331	2	SI21053
16	185	8.0	616	2	SI21053
17	183	7.9	292	2	SI21053
18	180	7.7	303	2	SI21053
19	180	7.7	608	2	SI21053
20	176	7.6	630	2	SI21053
21	173	7.4	918	2	SI21053
22	172.5	7.4	622	2	SI21053
23	170	7.3	897	1	SI21053
24	168	7.2	396	2	SI21053
25	163	7.0	830	2	SI21053
26	162.5	7.0	333	2	SI21053
27	161.5	6.9	1092	2	SI21053
28	161.5	6.9	719	2	SI21053
29	158	6.8	378	2	SI21053
30	157	6.8	896	1	SI21053
31	156.5	6.7	378	2	SI21053
32	154.5	6.6	896	2	SI21053
33	149	6.4	878	1	SI21053
34	146.5	6.3	608	2	SI21053
35	145	6.2	638	2	SI21053

36	145	6.2	638	2	SI21053	somatotropin recep
37	144.5	6.2	1097	2	SI21053	leukemia inhibitor
38	144	6.2	918	2	SI21053	interleukin-6 sign
39	142.5	6.1	917	2	SI21053	glycoprotein 130
40	141	6.1	638	2	SI21053	somatotropin recep
41	140	6.0	638	2	SI21053	somatotropin recep
42	139	6.0	508	1	SI21053	erythropoietin rec
43	139	6.0	634	2	SI21053	somatotropin recep
44	135.5	5.8	286	2	SI21053	granulocyte-macrop
45	134.5	5.8	557	2	SI21053	interferon alpha I

## ALIGNMENTS

RESULT 1  
SI2357  
Interleukin-5 receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Mar-1998  
C:Accession: SI2357  
R:Takaki, S.; Tomimaga, A.; Hiroshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu  
OMBO J. 9, 4367-4374, 1990  
#Title: Molecular cloning and expression of the murine interleukin-5 receptor.  
#Reference number: SI2357, MIDB:91092260  
#Accession: SI2357  
#Status: preliminary  
#Molecule type: mRNA  
#Residues: 1-415 <TAK>  
#Cross-references: GB:090205; NID:9220465; PID:d1014936; PID:9220466  
#Keywords: cytokine receptor; transmembrane protein

Query Match 13.7%; Score 318; DB 2; Length 415;  
Best Local Similarity 23.9%; Pred. No. 1.6e-17;  
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

QY 33 PPTNLSVSEVNCCTVMTWNP-PEGASSNCSLWFSHF-GDKDKKIADETRSEVPL 90  
DB 29 PPTNLSVSEVNCCTVMTWNP-PEGASSNCSLWFSHF-GDKDKKIADETRSEVPL 87

QY 91 NERICLQVSGSCSTNESEKPSILVEKICSPEDDPESAVTELQICIMHNL----- 140  
DB 88 HEGFASVRLTKSSHTLSSVMSAELKAPGSPGTSVNLCTHTVSSHTLRPYQ 147

QY 110 SYKCSWLPGRNTSPDTNITLYTHNSLEKIHOCENTFR--GQYECSDLRKXDSF 137  
DB 148 VSLRCTLVGLKDAEDTQYLYRFGVLE--KCOEYSRDLNRRNTACWPFRTFINSKGF 205

QY 198 EOHVSVOHVADMGKIKPSNIYPLTSRVKPDPPHKNLSFHNDDLYQWENRQN-FISR 256  
DB 206 EOLVFTINGSSKRAILFFQDLSPALIDQVNPRTVYIESNLTQWEKLSAPPDH 265

QY 257 CLFYEVENNSQTEHNHFVVOEAKCENPEFRNVENTSCFVMPGVLPDLNTRIVKVT 316  
DB 266 CFVNEKLYITKNG-----HIQKEKLIANFKIDVSVY-----SIQVRAAV 309

QY 317 NKLCYEDKLSWMSQMSGKRNSTLYTLLIYVYAGAIYVLLYLAKLKII--- 374  
DB 310 SSSCPMPGR-WGEMSOPIYVGERKS-LVEMHLIVP---TAACFVLLIRSLICRCHLW 364

QY 374 --TFPPDPGKIFKEMFGQNDLHWKVDLYEQTRETSVY 417  
DB 365 TRLEPPVAPKSNIKDL-----PVTEYERPSNETKIEVV 399

RESULT 2  
SI21052  
Interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Feb-1998  
C:Accession: SI21052; A46175  
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.







```
OY      321 YEDDKLWMSQEMSGKKRNS--TLXITMLIVPIVYGAILLYLKRLKI-IIIPP 377  
        ||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      305 N-----MSSMSAIERGSDGNGSLGYIYLVLIVGLVAGC-IVLGELFRFRLRIQLRPFP 358  
  
OY      378 IDPDGKIRFMFGDON--DDTILHMKKYDIYE-KQTKEETDSV 416  
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db      359 VPO---IKDKLNHNHEVEDEIIWEFTPEEGKGREEVLTV 396  
  
RESULT          7  
A55718  
interleukin-2 receptor gamma chain precursor - dog  
C:Species: Canis lupus familiaris (dog)  
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999  
C:Accession: A55718  
R:Henthorn, P.S.; Somberg, R.L.; Famlani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg,  
Genomics 23, 69-74, 1994  
A>Title: IL-2/Bgamma gene microdeletion demonstrates that canine x-linked severe combined  
A:Reference number: A55718; MUID:95130114  
A:Accession: A55718  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-373 <HEN>  
A:Cross-references: GB:IU04361; NID:g517411; PIDN:AAC48403.1; PID:g517412  
C:Superfamily: interleukin-2 receptor gamma chain  
C:Keywords: cytokine receptor; duplication
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Query Match	8.9%	Score 207;	DB 2;	Length 373;
Best Local Similarity	25.1%;	Pred. No. 7.1e-09;		
Matches 76;	Conservative 52;	Mismatches 131;	Indels 44;	Gaps 14

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QY      88  VPLNERICLOQWOCSTNESEKPSILVEKICISPPGDEBSATELLOCIAMHNSYKKSML 147
Dh      21  VGLNSTVMPNG-----NEDITPDEFILATPSETILSVSSILPEVQOCVFNVEYINACTWN 75
QY      148  PGRNTSPNTNTLYIWAHSL--EKIHOCEN-IFREGQYFGCSFDITKVKDSSFQHSVOI 204
Dh      76  SSSEBRP-TNLTLLHWYNSNDKQVOECGHLLFSREVTAGCW--LQKEEILLYEFVQOL 132
QY      205  MYKNAGKIKPSFNVLPTSRYKPPPHIKNLSFNH--DDLTYQWENHPQNFISRCLEYE 261
Dh      133  --RDRPRRROSTQKRLKQNLVIYMAP--ENULTLNLSQSULELSWSN--RHLDHCLHEV 186
QY      262  VEYNNQSQTEIHNVFYOEACENPEFERNVENTSCEFAVGYLPLDTLNTVIRVATNKLYC 321
Dh      187  VOYRSDMDRST-----EQSVDRHSFSFLPSVDGQKFTYFRVRSRYNPLCG 232
QY      322  EDDRLKSNWSQEMSIGK--KRNSTLYITMLIPIVYIATIVLL--LYKRLKLTIFP 376
Dh      233  SAQR-WBSMSHPIMGNTSKENPLFASAEAVLIFLGSGLITISLCIYWTLEP-----SIP 287
QY      377  PIP 379
Dh      288  RIP 290

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RESULT 8  
I49280  
Interleukin-2 receptor gamma chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Feb-1997 #sequence,revision 27-Feb-1997 #text,change 23-Jul-1999  
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53598  
R:Cao, X.; Kozak, C.A.; Liu, Y.  
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993  
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gene  
A:Reference number: A47514; MUID:3391374  
A:Accession: I49280  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-369 <CAO>  
A:Cross-references: EMBL:U01795; NID:g727349; PIDN:AAA64279.1; PID:g727350  
A:Accession: A47514

A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-369 <RES>  
A:Cross-references: GB:IL20048; NID:g404067; PIDN:AAA39286.1; PID:g404068  
R:Kiwaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamuta, K.  
Biochem. Biophys. Res. Commun. 193, 356-363, 1993  
A>Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of five  
A:Reference number: JN0592; MUID:933277575  
A:Accession: JN0592  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-369 <KIM>  
A:Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:d1003265; PID:g30303  
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.  
Gene 130, 303-304, 1993  
A>Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.  
A:Reference number: JN0775; MUID:93366191  
A:Accession: JN0775  
A:Molecule type: mRNA  
A:Residues: 1-369 <KOB>  
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:d1003480; PID:g436044  
R:Chiu, R.K.; Dougherty, G.J.  
submitted to the EMBL Data Library, October 1993  
A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain  
A:Reference number: S97582  
A:Accession: S37582  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>  
A:Cross-references: EMBL:X75337  
R:D'Amato, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de  
Eux, J. Immunol. 24, 3014-3018, 1994  
A>Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal  
A:Reference number: 153398; MUID:95104285  
A:Accession: 153398  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-369 <RES>  
A:Cross-references: GB:S75852; NID:g661554; PIDN:AAB32904.1; PID:g661555  
C:Genetics:  
A:Gene: IL-2rgamma  
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3  
A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta  
epitopes.  
C:Function:  
A:Description: receptor for interleukin-2  
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N  
C:Superfamily: interleukin-2 receptor gamma chain  
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:2-366/Product: interleukin-2 receptor gamma chain #status predicted <MAT>  
F:256-264/Domain: transmembrane #status predicted <TM>  
F:71/75,84,96,159,164,306/Binding site: carboxydrate (Asn) (covalent) #status predict

```

0Y 103 STNSEKRSITVEKICISPPEDDEPSAATLOQJWNNHNSYKNCMWLGRRNSPD---TNYT 159
D5 31 SANDICADILITJTADEHLSAPLTLPLEVOQCFVFNENYNCMW---NSSSPQATNLT 86
0Y 160 LYUHHRSLEKIHOCENIFREGQYFGCSFDLTUKKXDSSEFQHSQV-----IMKDNAGKT 213
D5 87 LHYRYKXSD-----NNFQOCSHYLSKEIT--SGQIQOEDQLQYQTFVVOLOQDPQKPQ 139
0Y 214 KPSENIPLTSRYKPDPPHIKNLSFHN---DLYVOWMENQNFISKRLCFEVEVNNSSQTE 270
D5 140 RRAVQKLNQNLVYPRAP--ENLJLSLSSQJELNRKS--RHJKEKQLOLYVYRSNRDR 196
0Y 271 THNYFYQEKACENPEPERVENVENTSCPMVGVLPDLTN--TVIRVKTNKLCEYEDDKLWS 328

```

Db 197 SWT-----ELIYNHREFSLPSV--DELKRYTFRVRSKYNPICGSSOO-WS 239

QY 329 NMSEMSIGK---KRNSTLITMILIVPAGAIIVLL---YLKRLKIIIFPIIDPG 382

Db 240 KMSOPVHMSHYEENSLEALNVLIPVGMGLITLILFYCWLENN-----PIIP-PI 293

QY 383 KIFKEMFGDONDDTLHW 399

Db 294 KNLDELTEYOGNFSAN 310

RESULT 9

A42565

Interleukin-2 receptor gamma chain - human

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1993

C:Accession: A42565; A46591; 154332

R:Takekoshi, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.; Science 257, 379-382, 1992

A:Title: Cloning of the gamma chain of the human IL-2 receptor.

A:Reference number: A42565; M01D:92335883

A:Accession: A42565

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid; protein

A:Residues: 1-369 <FAK>

A:Cross-references: GB:D11086; NID:q303611; PIDN:BA01857.1; PID:di002334; PID:g219890

A:Experimental source: MOLT beta lymphoid cells

A:Note: sequence extracted from NCBI database (NCBIP:109167)

R:Koguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.

J. Biol. Chem. 268, 13601-13608, 1993

A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.

A:Reference number: A46591; M01D:93293887

A:Accession: A46591

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: GB:J12183; NID:q307056; PIDN:AA59145.1; PID:q307058

R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Wallard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993

A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked

A:Reference number: I54332; M01D:94004847

A:Accession: I54332

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RE2>

A:Cross-references: GB:J19546; NID:q349631; PIDN:AAC37524.1; PID:q349632

C:Genetics: SCID1; IMD4

A:Gene: GDB:11283; OMIM:308380

A:Cross-references: GDB:11283; OMIM:308380

A:Map position: Xq13.1-Xq13.1

A:Intons: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3

A:Note: defects are associated with an X-linked form of severe combined immunodeficiency

C:Superfamily: Interleukin-2 receptor gamma chain

C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunodeficiency

Query Match 8.7% Score 202; DB 2; Length 369;

Best Local Similarity 27.2%; Pred. No. 1.7e-08; Indels 48; Gaps 14;

Matches 72; Conservative 44; Mismatches 101;

QY 131 ELQCIHNLNLMKCSWLPGRNTSPDNTLYLWIRSL--EKIHOCEN-IFREGOYFGCSF 187

Db 59 EVGCEVNEVNMCTNMSSEPOQ-TNLTLHYWKNSDKNDKVCCHYLSEITSGC-- 116

QY 188 DLKRVDSFEQHSVOQIMVNDNAGKIKPSFNIVPLTSRVAPDPPIHNLNLSFH--ANDLY 244

Db 116 QLOKKEHLVQTFVYOL--ODPREPRQATQOMKLOLVIPMAV--DNLTLLHKLSESOLE 171

QY 245 VQENPONTISRCI---FYEVEVNSQTEHNVFYQEAKECEPEREVENVENTSCFMP 300

Db 172 LAMNN--RFLNHLLEHLYQRTMDHSHWT-----EQSVDRHAKFSLP 211

QY 301 GVLDPDLNTVIRIKVTKNLCEYEDDKLMSNMSOEMSIG--KRNSTLYITMLIVPIVA 357

Db 212 SVSCKRYTFRVRSRNPFLC-GSAQHWSEWSHPIMQSNMNSKEPFLFALEAVYISVSM 270

QY 353 GATVLL---LYLRLKIIIFPIIP 379

Db 271 GLIISLLCYFWLER---TMPRIIP 291

RESULT 10

J01655

prolactin receptor precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 10-Sep-1997

C:Accession: J01655

R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.; Biochem. Biophys. Res. Commun. 180, 490-496, 1992

A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA

A:Reference number: J01655; M01D:93075121

A:Accession: J01655

A:Molecule type: mRNA

A:Residues: 1-831 <TAN>

A:Cross-references: DBJ:DJ3154; NID:q222848; PID:di002939; PID:g222849

A:Experimental source: kidney

C:Keywords: glycoprotein; transmembrane protein

F:1-23/Domain: signal sequence #status predicted <Sig>

F:24-831/Product: prolactin receptor #status predicted <MAT>

F:439-462/Domain: transmembrane #status predicted <TM>

F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 8.5% Score 197.5; DB 2; Length 831;

Best Local Similarity 23.1%; Pred. No. 1.1e-07;

Matches 91; Conservative 59; Mismatches 159; Indels 85; Gaps 19;

QY 32 QP--PTNLSVSVENICTV--IWT-MNP--EGASSNCSIMYFSGDKODKRIAPETR 84

Db 126 QPSPV-NLTLETKRSANIMYLMKMSPLADASSN---HLVHY---ELRIKPEKE 176

QY 85 SIYPLNERICLOVSGCSNNE-----SKRSLIVKCSPP 121

Db 177 EWEI---ISVGVOYQCKIKRLNLAGNRYVQYCTIDPEGSEWSESRHLLIPSGOSP 231

QY 122 EGPDESIVTELQCIHNLNLMKCSWLPGRNTSPDNTLYLWIRSL--EKIHOCEN-IFREGO 181

Db 232 E-----KPTIIRKSPKKEFTCKMKRGDGHPTNTLLXSGEGEYVCEPD-YITAG 285

QY 183 YFGCSFDLIRVKSSEFQHSVOQIMVNDNAGKIKPSFNIVPLTSRVKDPD---HIKNT 236

Db 286 PNCGYFD--KKHNSFWTIVNIVRATNEMGSNSDPHYVDVTIYVQDPDPVNTLLEKRP 343

QY 237 SFHNDLIVQENPONTISR---CLFEVEVNSQTEHNVFYQEAKECEPEREVENVE 292

Db 344 INRPVYVLTWSPPLADVSGMLTLEELRLKPEESEELETFVQ-QYQYKFSLN-- 401

QY 293 NTCSEMPVGLPDLNTVIRIKVTKNLCEYEDDKLMSNMSOEMSIGKRNSTLYITMLIV 352

Db 401 -----PKKVIYIQHCKP-----DHRGSMSESENITQIPNDPRVDMIVIV 444

QY 353 PVIVAGAIIVL---LYLRLKIIIF--PIIPDP 381

Db 445 LGVLSLLICLINSMTWLKGYRMTFLPVPGP 478

RESULT 11

A34631

lactogen receptor 1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jul-1990 #sequence\_revision 09-Oct-1992 #text\_change 10-Sep-1997

C:Accession: A34631

R:Zhang, R.; Buckko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.; Biochem. Biophys. Res. Commun. 168, 415-422, 1990

A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cD

A:Reference number: A34631; M01D:90241201

A:Accession: A34631  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-610 <ZNA>  
 A:Cross-references: GB:M4083; NID:9205122; PID:9205123  
 A:Note: the authors translated the codon GAG for residue 533 as G1Y

Query Match 8.1%; Score 190; DB 2; Length 610;  
 Best Local Similarity 23.7%; Pred. No. 2.9e-07;  
 Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KPSILVEKICSPEDPSAVTELOCIWNLNLYKMSMLPGRNTSPDNTLYLWHRSL 168  
 DB 25 KPEI--HKCRSP--DKET-----FTCMWNPCTDGLPTNLSLYSKRGEK 65  
 QY 169 KIHOCENFRGOYFGSGFDLTKYKDSFEQHSQVIMKDNAGIKRSENVPLTSRVPK 228  
 DB 66 TTYECPPDKTSQPN--SCFF--SKOYTSIMKIYIITVNATNOMGSSSDPLYVDVYIYEP 122  
 QY 229 DPP-----HIKNSLFHNDILYVOMENPQNFISR-----CLFEVEVNNSSQTEHNAVYOE 279  
 DB 123 EPPNMLTEVQOLKDKRTYLMVKMSPTIIDVKTGWTMEYELRLKEEAEWEIHF--- 180  
 QY 280 AKCENPEERENVNTSCFMPGVLPTLNTVRIRVKTNKLCEYEDDKLMSWQSEMSIGKK 339  
 DB 180 -----TGHOITQFKVFDLYPGQKYLQYTR-----CKPDHGYSRMSQSSSEVEMP 222  
 QY 340 RNSTLYITMLIIVVAGAIIVLLYLKRLK-----IIFPPIDP 381  
 DB 223 NDFLTKDTIWIITAILSAVICLIIMWAVALKGYSMTCTIFFPVPGP 269

## RESULT 12

A36116  
 prolactin receptor 2 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 10-Sep-1997  
 C:Accession: A36116  
 R:Shiota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boulton, J.M.; Edey, M.; Djiane, J.  
 M.O. Endocrinol. 4, 1136-1143, 1990  
 A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.  
 A:Reference number: A36116; MUID:91155946  
 A:Accession: A36116  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-610 <SHI>  
 A:Cross-references: GB:M57668; NID:9206366; PID:9206367; GB:M60728

Query Match 8.1%; Score 189; DB 2; Length 610;  
 Best Local Similarity 23.7%; Pred. No. 3.4e-07;  
 Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KPSILVEKICSPEDPSAVTELOCIWNLNLYKMSMLPGRNTSPDNTLYLWHRSL 168  
 DB 25 KPEI--HKCRSP--DKET-----FTCMWNPCTDGLPTNLSLYSKRGEK 65  
 QY 169 KIHOCENFRGOYFGSGFDLTKYKDSFEQHSQVIMKDNAGIKRSENVPLTSRVPK 228  
 DB 66 TTYECPPDKTSQPN--SCFF--SKOYTSIMKIYIITVNATNOMGSSSDPLYVDVYIYEP 122  
 QY 229 DPP-----HIKNSLFHNDILYVOMENPQNFISR-----CLFEVEVNNSSQTEHNAVYOE 279  
 DB 123 EPPNMLTEVQOLKDKRTYLMVKMSPTIIDVKTGWTMEYELRLKEEAEWEIHF--- 180  
 QY 280 AKCENPEERENVNTSCFMPGVLPTLNTVRIRVKTNKLCEYEDDKLMSWQSEMSIGKK 339  
 DB 180 -----TGHOITQFKVFDLYPGQKYLQYTR-----CKPDHGYSRMSQSSSEVEMP 222  
 QY 340 RNSTLYITMLIIVVAGAIIVLLYLKRLK-----IIFPPIDP 381  
 DB 223 NDFLTKDTIWIITAILSAVICLIIMWAVALKGYSMTCTIFFPVPGP 269

## RESULT 13

A41070  
 prolactin receptor Nb2 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 10-Sep-1997  
 C:Accession: A41070; 155417  
 R:Ali, S.; Pellegrini, I.; Kelly, P.A.  
 J. Biol. Chem. 266, 20110-20117, 1991  
 A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin receptor.  
 A:Reference number: A41070; MUID:92041834  
 A:Accession: A41070  
 A:Molecule type: mRNA  
 A:Residues: 1-412 <ALI>  
 A:Cross-references: GB:M74152; NID:9206389; PID:9206390  
 R:O'Neal, K.D.; Yu-Lee, L.Y.  
 J. Biol. Chem. 269, 26076-26082, 1994  
 A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor.  
 A:Reference number: 155417; MUID:95014432  
 A:Accession: 155417  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-412 <RES>  
 A:Cross-references: EMBL:U07567; NID:9641963; PID:9641964  
 A:Experimental source: Nb2-11C cell line  
 C:Keywords: transmembrane protein

Query Match 8.1%; Score 189; DB 2; Length 412;  
 Best Local Similarity 23.7%; Pred. No. 2.1e-07;  
 Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KPSILVEKICSPEDPSAVTELOCIWNLNLYKMSMLPGRNTSPDNTLYLWHRSL 168  
 DB 25 KPEI--HKCRSP--DKET-----FTCMWNPCTDGLPTNLSLYSKRGEK 65  
 QY 169 KIHOCENFRGOYFGSGFDLTKYKDSFEQHSQVIMKDNAGIKRSENVPLTSRVPK 228  
 DB 66 TTYECPPDKTSQPN--SCFF--SKOYTSIMKIYIITVNATNOMGSSSDPLYVDVYIYEP 122  
 QY 229 DPP-----HIKNSLFHNDILYVOMENPQNFISR-----CLFEVEVNNSSQTEHNAVYOE 279  
 DB 123 EPPNMLTEVQOLKDKRTYLMVKMSPTIIDVKTGWTMEYELRLKEEAEWEIHF--- 180  
 QY 280 AKCENPEERENVNTSCFMPGVLPTLNTVRIRVKTNKLCEYEDDKLMSWQSEMSIGKK 339  
 DB 180 -----TGHOITQFKVFDLYPGQKYLQYTR-----CKPDHGYSRMSQSSSEVEMP 222  
 QY 340 RNSTLYITMLIIVVAGAIIVLLYLKRLK-----IIFPPIDP 381  
 DB 223 NDFLTKDTIWIITAILSAVICLIIMWAVALKGYSMTCTIFFPVPGP 269

## RESULT 14

A29884  
 prolactin receptor precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 20-Mar-1998  
 C:Accession: A29884  
 R:Boulton, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edey, M.; Shiota, M.; Banville, J.  
 Cell 53, 69-77, 1988  
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth factor receptor family.  
 A:Reference number: A29884; MUID:88165059  
 A:Accession: A29884  
 A:Molecule type: mRNA  
 A:Residues: 1-310 <BOU>  
 A:Cross-references: GB:M19304; NID:9206364; PID:9206365  
 C:Keywords: transmembrane protein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-310/Product: prolactin receptor #status predicted <MAP>

Query Match 8.1%; Score 189; DB 2; Length 310;  
Best Local Similarity 23.7%; Pred. No. 1.4e-07;  
Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

Search completed: January 19, 2000, 14:58:50  
Job time: 3635 sec

QY 109 KPSILVEKCISSPEGDESAVTELOCIMHNLSTYKCSMLGCRNTSPDNTLYYHRSLE 168  
DB 25 KPEI--HKCRSP--DKET-----FTCMWNPETDGLPTNYSLTYSKEGEK 65  
QY 169 KIHOCENIFREGQFGCSFDLTWKYKSSFEHOSVOIMVKDAGKIKPSFNIVPLTSRVPK 228  
DB 66 TTYECPDKTSGPN--SCFF--SKQYTIWKIYITVNATNOMGSSSDPLVDYVYIEP 122  
QY 229 DPP-----HIKNLSFHNDLYVQWENPQNFISR---CLFEYEVNNSQETNHFVVOE 279  
DB 123 EPPRNLLLEVKQKDKKTYLWVKMSPTLIDVKGTGFTMEIRLKPDEAEWEIHF--- 180  
QY 280 AKCENPEFERNVENTSCFPMVPGVLPDLNTVIRVKTNKLCEYEDDKLSMNSQEMSIGKK 339  
DB 180 -----TGHOTQFKYFDLPGOKYLYQTR-----CKPDHGYSRWSQESSVEMP 222  
QY 340 RNSTLYITMLIIVPVIVAGAIIVLLYLKRLK-----IIFPPIDP 381  
DB 223 NDFTKDTYWTIYAILSAVICIMWAVALKGYSMTCLIFPVPGP 269

## RESULT 15

I45971  
prolactin receptor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 28-Feb-1997  
C:Accession: I45971  
R:Scott, P.; Kessler, M.A.; Schuler, L.A.  
Mol. Cell. Endocrinol. 89, 47-58, 1992  
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin  
A:Reference number: I45971; M01D:33246019  
A:Accession: I45971  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-581 <SC0>  
A:Cross-references: GB:I02549; NID:g163617; PID:g163618  
C:Genetics:  
A:Gene: PRLR

Query Match 8.0%; Score 186; DB 2; Length 581;

Best Local Similarity 24.3%; Pred. No. 5.6e-07;  
Matches 80; Conservative 44; Mismatches 115; Indels 90; Gaps 16;

QY 108 EKPSILVEKCISSPEGDESAVTELOCIMHNLSTYKCSMLGCRNTSPDNTLYYHRSLE 167  
DB 29 EKPKLV--KCRSPK-----EFTCMWNEGAGGLPTNITLYYHKEGE 69  
QY 168 EKHOCENIFREGQFGCSFDLTWKYKSSFEHOSVOIMVKDAGKIKPSFNIVPLTSRVPK 227  
DB 70 TLHHECPD--YKTGPNCSYF--SKKHTSIWKMYITVNAINOMGISSDPLVHYIYIE 126  
QY 228 PDPPIKNSL--HND-----LYVQWENPQN-----FISRLFEYEVNNSQET---E 270  
DB 127 PEPP--ANLTLELKHPEKRPYTLWKMSPTMIDVKSGMT--IYETIRLKPDEKADWE 181  
QY 271 THNFYVQAEKCNPEFERNVENTSCFPMVPGVLPDLNTVIRVKTNKLCEYEDDKLSMNSW 330  
DB 182 THFTLKOTQKIFN-----LYGQKYLYQIR-----CKPDHGYSSEW 218  
QY 331 SQEMSTGKRNSTLYITMLIIVPVIVAGAIIVLLYLKRLK-----IIFPPIDPDKIF 385  
DB 219 SPESIOIPNDFPVKDSMIFVALISAVICIMWAVALKGYSMTCLIFPVPGP--KI- 277  
QY 386 KEMFGQNDOTLHWKRYDIY--EKQTKEE 412  
DB 277 -----KGFVHLEKGSSE 291

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OM protein - protein search, using sw model

Run on: January 20, 2000, 06:19:55 ; Search time 35.05 Seconds

(without alignments)  
354.343 Million cell updates/sec

Title: US-09-077-817-4

Sequence: 1 MEMPARLCGLNALLCAGCG.....QTKETDSVLIENIKKASQ 427

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database: SwissProt\_38.\*

Word size: 0

Number of hits that pass the threshold: 80000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2324	100.0	427	1131_HUMAN	P78552 homo sapien
2	1698.5	73.1	424	1131_MOUSE	O09030 mus musculu
3	318	13.7	415	1131_MOUSE	P21183 mus musculu
4	296.5	12.8	420	1131_MOUSE	O01344 homo sapien
5	295.5	12.7	380	1132_HUMAN	O14627 homo sapien
6	228	9.8	400	1132_HUMAN	P15509 homo sapien
7	207	8.9	373	1132_HUMAN	P40321 canis famill
8	205.5	8.8	369	1132_HUMAN	P34902 mus musculu
9	202	8.7	369	1132_HUMAN	P31785 homo sapien
10	198.5	8.5	831	1132_HUMAN	O21094 meleagris g
11	197.5	8.5	831	1132_HUMAN	O04594 gallus gall
12	197	8.5	379	1132_HUMAN	O95118 bos taurus
13	189	8.1	610	1132_HUMAN	P05710 rattus norv
14	186	8.0	581	1132_HUMAN	O28172 bos taurus
15	185	8.0	616	1132_HUMAN	P14787 oryctolagus
16	180	7.7	608	1132_HUMAN	O08501 mus musculu
17	176	7.6	630	1132_HUMAN	O91513 oryctolagus
18	173	7.4	918	1132_HUMAN	P40189 homo sapien
19	172.5	7.4	622	1132_HUMAN	P16771 homo sapien
20	168	7.2	396	1132_HUMAN	P32927 homo sapien
21	168	7.2	396	1132_HUMAN	P26952 mus musculu
22	163	7.0	830	1132_HUMAN	O90374 columba liv
23	162	7.0	581	1132_HUMAN	O28235 cervus elap
24	161.5	6.9	378	1132_HUMAN	P42703 mus musculu
25	158	6.8	396	1132_HUMAN	P26951 mus musculu
26	157	6.8	396	1132_HUMAN	P26955 mus musculu
27	149	6.4	878	1132_HUMAN	P26952 mus musculu
28	146.5	6.3	608	1132_HUMAN	O02092 gallus gall
29	145	6.2	634	1132_HUMAN	P79108 bos taurus
30	145	6.2	638	1132_HUMAN	P10912 homo sapien
31	144.5	6.2	1097	1132_HUMAN	P42702 homo sapien
32	144	6.2	918	1132_HUMAN	P40190 rattus norv
33	142.5	6.1	917	1132_HUMAN	O00560 mus musculu
34	141	6.1	611	1132_HUMAN	O90375 columba liv
35	141	6.1	638	1132_HUMAN	P19756 sus scrofa
36	140	6.0	638	1132_HUMAN	P19941 oryctolagus
37	139	6.0	508	1132_HUMAN	P19235 homo sapien
38	139	6.0	634	1132_HUMAN	O28575 ovis aries
39	135	5.8	638	1132_HUMAN	P79194 macaca mula

## ALIGNMENTS:

RESULT	1	STANDARD	PR	427 AA
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AC	P78552: 099656:			
DT	01-NOV-1997 (rel. 35, Created)			
DT	01-NOV-1997 (rel. 35, Last sequence update)			
DT	15-JUL-1999 (rel. 38, Last annotation update)			
DE	INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1)			
GN	IL13RA1 OR IL13RA OR IL13R.			
CS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
CC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-CARCINOMA:			
RX	MEDLINE: 97165986			
RA	MILLOUX B., LAURENT P., BONNIN O., LUPKER J., CAPUT D., VITA N., FERRARA P.,			
RT	"Cloning of the human IL-13R alpha1 chain and reconstitution with the IL13R alpha of a functional IL-4/IL-13 receptor complex."			
RV	FEBS Lett. 401:163-166(1997).			
RN	[12]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-B-CELL:			
RA	GAUDHAT J.F.M., SCHLAGENHAUF E., FENG N.P., MOSER R., YAMAGI M., JEANIN P., ALLOUINI S., ELSON G., NOTARANGELO L.D., WELLS T., EUGSTER H.P., BONNEPOY J.Y.,			
RT	Submitted (Jan-1997) to the EMBL/Genbank/DBD databases.			
RN	[13]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-T-CELL:			
RX	MEDLINE: 97067184.			
RA	AMAN M.J., TAYEBI N., OBIRI N.I., PURI R.K., MODI W.S., LEONARD W.J.,			
RT	"cdna cloning and characterization of the human interleukin 13 receptor alpha chain."			
RV	J. Biol. Chem. 271:29265-29270(1996).			
CC	- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA C.			
CC	- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.			
CC	- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER, SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.			
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
CC	- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
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CC	EMBL, Y10659; CAA71669.1;			





Query Match	13.7%	Score 318;	DB 1;	Length 415;
Best Local Similarity	23.9%	Pred. No. 2,4e-17;		
Matches	97;	Conservative	74;	Mismatches 179; Indels 56; Gaps 14;
01 CARBOHYD	32	32	POTENTIAL.	
02 CARBOHYD	128	128	POTENTIAL.	
03 CARBOHYD	213	213	POTENTIAL.	
04 CARBOHYD	241	241	POTENTIAL.	
05 SEQUENCE	415 AA;	46989 MW;	415Da67	CRC32;
06 Query Match	13.7%	Score 318;	DB 1;	Length 415;
07 Best Local Similarity	23.9%	Pred. No. 2,4e-17;		
08 Matches	97;	Conservative	74;	Mismatches 179; Indels 56; Gaps 14;
09 33 PPTVLSVSVENLCVITWNP-PEGASSNCSLMTFSHF-GDKQDKTAPETRSIEVPL	90			
10 29 PPV-NEFTKATGLAIVLLHMDPNPOEDORHVDLEHVAINAQEDEDYDTRKTESKCVPL	87			
11 91 NERILGCGSCSTSESEKPSILVEKSCSPREGDESAVTELOCIMHNH-----	140			
12 88 HEGPAASVNTIIKSSHTLLASWSAEIKAPGSGTSTNLCTGTHVYSSHTLPRQ	147			
13 140 SYMCSVLPGRNTSPDTNTLYLWRSLEKIHOCENFRE-GGYGSGSFDLTAKVDSF	197			
14 148 VSLRCTLVGNKRAPEDTQYFLYRFGVLTE-KQGEYSNDALNRTACMFRTFINSKGF	205			
15 09 ECHSVQVWKDNAGIKKSFNVLPLTSRYKPPPIKNSLSPNDLIYQWENPQN-FLSR	256			
16 206 EQLAHINGSSRAIKPFDDLFSLADQVPPRNVAVEIESNSLIQWENPLSAFPDH	265			
17 257 CLVEVEVNNSTETHANFEVQAEACENDEPERNVENTSCFVWPGVLPDLTLVTRIVKT	316			
18 266 CFNYELKTIYNTNG-----HIQEKYLIANKPISKIDDDVY-----SIQYRAV	309			
19 07 NKLLYEDDKLMSNMSQESIGKRRNSTLYITMLLIVPIVAGAILVLLYKRLKII---	374			
20 310 SSCPMPGR-MGEMSQPIYVGKERS-LVEMHLYLP--TAACVLLIFSLICVCHLM	364			
21 09 374 --IIFPIPDGKIFKEMFGDDNDLHMKKDIYKQKREEDSVV	417			
22 DL 365 TRLEPVPAPKSNKDL-----PVYTEKPSNEKIEVV	399			
23 RESULT 4				
24 IL5R HUMAN				
25 ID IL5R HUMAN	STANDARD:	PRT:	420 AA.	
26 AC 001344				
27 DT 01-JUL-1993 (Rel. 26, Created)				
28 DT 01-JUL-1993 (Rel. 26, Last sequence update)				
29 DT 01-NOV-1997 (Rel. 35, Last annotation update)				
30 DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125				
31 DE ANTIGEN)				
32 GY IL5RA OR IL5R.				
33 O3 Homo sapiens (Human).				
34 O3 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
35 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.				
36 [1]				
37 SEQUENCE FROM N.A.				
38 MEDLINE: 52372031.				
39 RA SCOTT H.S., GUO X.H., HOPWOOD J.J., MORRIS C.P.;				
40 "Structure and sequence of the human alpha-L-iduronidase gene.";				
41 RL Genomics 13:1311-1313(1992).				
42 [2]				
43 SEQUENCE FROM N.A.				
44 MEDLINE: 9235767.				
45 RA TAVERNIER J., TUYENS T., PLAETINCK G., VERHEE A., FLEERS W.,				
46 DEVOS R.;				
47 "Molecular basis of the membrane-anchored and two soluble isoforms of				
48 the human interleukin 5 receptor alpha subunit.";				
49 RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).				
50 [3]				
51 SEQUENCE OF 1-335 FROM N.A. (SI FORM).				
52 KA MEDLINE: 92035669.				
53 RA TAVERNIER J., DEVOS R., CORNELIS S., TUYENS T., VAN DER HEYDEN J.,				
54 FLEERS W., PLAETINCK G.;				
55 "A human high affinity interleukin-5 receptor (IL5R) is composed of				

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RT an IL5-specific alpha chain and a beta chain shared with the receptor
RT for GM-CSF.
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, TWO SOLUBLE FORMS AND A
CC MEMBRANE-BOUND FORM EXIST DUE TO ALTERNATIVE SPLICING OF THE
CC SAME GENE.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME-PROW; NOTE-CD guide Cdw125 entry;
CC WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm.
CC -----
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CC -----
CC EMBL; M96652; AAA59152.1; -
CC EMBL; M96651; AAA59151.1; -
CC EMBL; M75914; AAA36110.1; -
CC EMBL; A26249; CAA01793.1; -
CC EMBL; A24587; CAA01731.1; -
CC EMBL; A26251; CAA01794.1; -
CC PIR; A40267; A40267.
CC DR MIM; 147851; -
CC DR PROSITE; PS00241; RECEPTOR CYTOKINES_1; FALSE_NEG.
CC DR PROSITE; PS00340; RECEPTOR CYTOKINES_2; 1.
CC KM Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
CC FT CHAIN 1 20
CC FT SIGNAL 1 20
CC FT DOMAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
CC FT TRANSSEM 343 362 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 363 420 POTENTIAL.
CC FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 35 35 POTENTIAL.
CC FT CARBOHYD 131 131 POTENTIAL.
CC FT CARBOHYD 216 216 POTENTIAL.
CC FT CARBOHYD 244 244 POTENTIAL.
CC FT VARSPPLIC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).
CC FT VARSPPLIC 336 420 MISSING (IN SOLUBLE ISOFORM S1).
CC FT VARSPPLIC 333 333 N -> K (IN SOLUBLE ISOFORM S2).
CC FT VARSPPLIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
CC FT VARSPPLIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
CC SQ SPOUDENCE 420 AA: 47700 MW: 75C19847 CRC32:

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Query Match 12.88; Score 296.5; DB 1; Length 420;
Best Local Similarity 24.88; Pred. No. 1.1e-15;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

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QY 33 PVTNLSVSENLCTVMTWNP-PEGASSNCSLWYFHFQDKQDKTAPETRRSIEVPLN 91
QY 32 PVTNLSVSENLCTVMTWNP-PEGASSNCSLWYFHFQDKQDKTAPETRRSIEVPLN 91
QY 92 ERICLOV-----GSCSTNESEKPSILVEKICIS-----PPESDPSAVTELOCITMHLN--- 140
QY 83 ESKCVTLHKGFSAVITILIONDSILASSWASAEHLNAPSPGTSIYVNLCTNTTEDN 142
QY 140 -----SY-----MKSCMLGRNTPSPTNLYLYWHSLEKIHCCENIFER--GQYGGCSPDL 189
QY 143 YSRKRSQVSIHCHTWLGTDPEDTOFLYIRYSWTE--ECQYSSDTLRNIAWCPFR 200
QY 190 TKVDSSEFQHSVOIMKDNAGIKRPSINIVPLTSRYKPDPPHKNLSFHNDDLYVOMEN 249
QY 201 TFLSKGRDMLSVAVNNSKSAIRPFQDLALAIQINPLVNTVAIEGTRISIQMEK 260
QY 250 PGN-FISRCLEFVEVNNSTETHNVFYVOEAKENPFEERNVENTSCFVPGVLPDTLN 308

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DB 261 PVSAFPHCHDFEYKIKHNTBNG-----YLQIEKLMTNAFISIDLSKY----- 305
QY 309 TVAPRTVNTKCYEDDKKMSNCSGKRRSTLYITMLVPIYVAGAILVLLYLK 368
QY 305 DVQVRAVSSCKREAG-LNSENQPIYGVNDEKPLREMFVIMATTCILILSLICK 363
QY 369 --RLKIIIFPIPPDGKIFEMFGDONDDTLHWKKYDIYEKQTKRETSVYL 418
QY 364 ICHLMIKLFPPIAPSPNIMDLVTIN-----YKASSSEIELEVI 404
DB 364 ICHLMIKLFPPIAPSPNIMDLVTIN-----YKASSSEIELEVI 404
RECUIT 5
ID 1132 HUMAN STANDARD; PRT; 380 AA.
AC 014627; 000667.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13
DE BINDING PROTEIN).
GN IL13RA2 OR IL13R.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-RENAL CELL CARCINOMA;
RX MEDLINE, 96279273.
RA CAPUT D., LAURENT P., KAGHAD M., LELINS J.M., LEFORT S., VITA N.,
RA TERRANA P.
RT Cloning and characterization of a specific interleukin (IL)-13
RT binding protein structurally related to the IL-5 receptor alpha
RT chain.
RL J. Biol. Chem. 271:16921-16926(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA DONALDSON D.D., WHITERS M.J., FITZ L., NEBEN T., FINNERTY H.,
RA HENDERSON S.L., O'HARA R.M. JR., TURNER K.J., WOOD C.R., COLLINS M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA GUO J., MINVIELLE S.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13
CC (IL-13), BUT NOT TO IL-4.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL; X95302; CAA64617.1; -
CC EMBL; U70981; AAB17170.1; -
CC DR EMBL; Y08768; CAA70021.1; -
CC DR MIM; 300130; -
CC DR PRAW; PF00041; fn3; 1.
CC DR PROSITE; PS00340; RECEPTOR CYTOKINES_2; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 26
CC FT CHAIN 27 380 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN.
CC FT DOMAIN 27 343 EXTRACELLULAR (POTENTIAL).
CC FT TRANSSEM 344 363 POTENTIAL.
CC FT DOMAIN 364 380 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 145 155 BY SIMILARITY.

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FT DISULFID 184 197 BY SIMILARITY.  
 FT CARBOHYD 115 115 POTENTIAL.  
 FT CARBOHYD 215 215 POTENTIAL.  
 FT CARBOHYD 290 290 POTENTIAL.  
 FT CARBOHYD 299 299 POTENTIAL.  
 SQ SEQUENCE 380 AA: 44176 MW: 7234FEA4 CRC32;

Query Match 12.7% Score 295.5; DB 1; Length 380;  
 Best Local Similarity 26.0%; Pred. No. 1,2e-15;  
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 10 LMAALLCAGGGGGGGAAPETQPPVNTLSVSENLCTVIMTNPEGAS--SNCSLMYF 67  
 DB 11 LVFLSTGCGTSSSDTEIKVNPPODFELVDGVLGLVLOMOPSLDHFKECTVEY- 70  
 QY 68 SHGDKADKKIAPETRSI-----EVLNERICLOVGS-----OCSTNESKPSILV 114  
 DB 70 ----ELKRNIGSEWTWTITKMLHYKDGFDLNGKIEAKIHTLLPWOC--TNGSEVOSSMA 124  
 QY 115 EKC--ISPPGDEPSATLEQIMHNLSTYKCSMLPGRNTSPDNTLYXMHSLKTIHQ 172  
 DB 125 ETTYWIS--PGIPEKTKVODKCVYIMQYLCSMKPEIGVLDITNINLFTYIBGLHALQ 183  
 QY 173 C-ENIFREGQYFCSEFDLTKVKSDEPHSHVQIMVKNACKIRPSENIIVPLTSKXDPDP 231  
 DB 184 CVDYKADGNGICRPFYLEASD--YKDFYICVNGSSENNPISSTYTFQLQNIIVKPLP 241  
 QY 232 HINLSEFND---DLVQWENPONT--SRCLFEVEYVNSQTEHNVFYQEAKECPERF 287  
 DB 242 --VYLFTRSESEIKIKWISIPGPIPARCFDEIETREDDT-----LVATVENEY 293  
 QY 288 ERNVEVMS---CFMVGVLDPDLNTVIRKTKLCEDDKLSMNSQEM-----SIGRK 339  
 DB 294 TLKTYMETRQLCEVY-----RSKVNYIC--SDGINSSEMDCKWCEGEDISKR 339  
 QY 340 RNSTLYTMLIIVYVAGAIIVLLYLKRLKIIIPPIPDGKIFKEMFGD 391  
 DB 340 TLRFMLPF-----GFIILVIVTGL--LLRKPNTYP--KMIPEFCD 379

RESULT 6  
 GPCR\_HUMAN STANDARD: PRT: 400 AA.  
 ID GPCR\_HUMAN 014429; 014430;  
 AC P15509; 014429; 014430;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR RECEPTOR ALPHA  
 DE CHAIN PRECURSOR (GM-CSF-R-ALPHA) (CDW116) (CD116 ANTIGEN).  
 GN CSF2RA OR CSF2R.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A. (GM-CSF-R-ALPHA-1).  
 RC TISSUE-PLACENTA.  
 RA MEDLINE: 94368898.  
 RA HU X., EMANUEL P.D., ZUCKERMAN K.S.;  
 RA GEARING D.P., KING J.A., GOUGH N.M., NICOLA N.A.;  
 RT Expression cloning of a receptor for human granulocyte-macrophage  
 RT colony-stimulating factor.  
 RL EMBO J. 8:3667-3676(1989).  
 RP [2]  
 RP SEQUENCE FROM N.A. (GM-CSF-R-ALPHA-2 AND GM-CSF-R-ALPHA-3).  
 RC TISSUE-BLOOD.  
 RA MEDLINE: 94368898.  
 RA HU X., EMANUEL P.D., ZUCKERMAN K.S.;  
 RT Cloning and sequencing of the cDNAs encoding two alternative  
 RT splicing-derived variants of the alpha subunit of the  
 RT granulocyte-macrophage colony-stimulating factor receptor.  
 RL Biochim. Biophys. Acta 1223:306-308(1994).  
 RN [3]  
 RP SEQUENCE OF 1-385 FROM N.A.

RE MEDLINE: 94193800.  
 FA NAKAGAWA Y., KOSUGI H., MIYAJIMA A., ARAI K.I., YOKOTA T.;  
 RT Structure of the gene encoding the alpha subunit of the human  
 RT granulocyte-macrophage colony stimulating factor receptor.  
 RT Implications for the evolution of the cytokine receptor  
 RT superfamily.  
 RE J. Biol. Chem. 269:10905-10912(1994).  
 CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-STIMULATING  
 CC FACTOR.  
 CC -1- SUPPLEMENT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA  
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. GM-CSF-R-ALPHA-2  
 CC IS PROBABLY SOLUBLE.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS, GM-CSF-R-ALPHA-1 (SHOWN  
 CC HERE) TO GM-CSF-R-ALPHA-3, ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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 CC  
 CC EMBL: X17648; CAA35638.1; -  
 CC EMBL: D26628; BAA05656.1; JOINED.  
 CC EMBL: D26618; BAA05656.1; JOINED.  
 CC EMBL: D26619; BAA05656.1; JOINED.  
 CC EMBL: D26620; BAA05656.1; JOINED.  
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 CC EMBL: D26649; BAA05656.1; JOINED.  
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 CC EMBL: D26656; BAA05656.1; JOINED.  
 CC EMBL: D26657; BAA05656.1; JOINED.  
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 CC EMBL: D26666; BAA05656.1; JOINED.  
 CC EMBL: D26667; BAA05656.1; JOINED.  
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 CC EMBL: D26669; BAA05656.1; JOINED.  
 CC EMBL: D26670; BAA05656.1; JOINED.  
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 CC EMBL: D26674; BAA05656.1; JOINED.  
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 CC EMBL: D26680; BAA05656.1; JOINED.  
 CC EMBL: D26681; BAA05656.1; JOINED.  
 CC EMBL: D26682; BAA05656.1; JOINED.  
 CC EMBL: D26683; BAA05656.1; JOINED.  
 CC EMBL: D26684; BAA05656.1; JOINED.  
 CC EMBL: D26685; BAA05656.1; JOINED.  
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Query Match 9.8%; Score 228; DB 1; Length 400;  
 Best Local Similarity 22.4%; Pred. No. 1.9e-10;  
 Matches 90; Conservative 82; Mismatches 180; Indels 50; Gaps 18;

CC 31 TOPPVTNLISVENICTVIMTWNPPEGAS-SNCSLMYFSHRGKODKKIAPETRSTIEVP 89  
 DB 29 TVAPASSINIVRDSR-TYNLSMDCENTTFKCFI-----TDKKNVRELRSLNNECSC 81  
 CC 90 LNERCLOVGSOCSTNESEKRSILVEKICSPEDDPESATVLOCIMHNSYKCSWLPJG 149  
 DB 82 TFEICLHEGTEFEYHYVTSQGFQOKLIPNSGREGTAAQNFSCFTYNDLMNCWARG 141  
 CC 150 RNTSPDITVYLYWHRSLERKIHOCENIFRE-GOYFGCSFD-LIKVKSSEPHQVQIMVK 207  
 DB 142 PTAPRDVQYFLYINRSRRRIRCPYIYQDSGTGCHLNLSSLSRNY-----FLVN 195  
 CC 208 DNAGKIRSF-NIVPLTSRYKPPPHIKNLSEHNDLVYQWENPQNF-ISRCLEF-YEV 262  
 DB 196 GTSKEIGIOFDSLLDKTKIERFNPNSVTRCMTCHLRMKOPRTYOKLSTLDFOYOL 255  
 CC 263 EVN--NSQTEHNVFYQEAKECENPEFERNVENTSCMVGCVLPDLINTVIRKYNKLC 320  
 DB 256 DVHRKNTQPTENLLINVSGLDNR-----YNPSSPRAKSHSVKIRADVRIL 304  
 CC 321 YEDDKLSMNSOEMSICKRNS--LYITMLLIPYIVAGAILVLLYKRLKI-IIIPP 377  
 DB 305 N-----WSSWSEAEIEFGSDGNGSVIYVLLIVGLVYG-IVLGLFRLRIQIRLFP 358  
 CC 378 IPPGKIRKFMFGDON--DPTLHKKKYDIYE-KQTEEDSV 416  
 DB 359 VPQ-----IKDKLNDNHEVEDEITWEETPEEGKGYREVLTV 396

RESULT 7  
 CTRG\_CANFA  
 ID CTRG\_CANFA STANDARD; PRT: 373 AA.  
 AC P40321;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).  
 GN IL2RG.  
 OS Canis familiaris (Dog).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
 CC Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SPLEEN;  
 RX MEDLINE: 95130114.  
 RA HENTHORN P.S., SOMBERG R.L., FIMANT V.M., PUCK J.M., PATTERSON D.F.,  
 RA FELSBURO P.J.;  
 RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked  
 RT severe combined immunodeficiency is a homologue of the human  
 RT disease.";  
 RL Genomics 23:69-74(1994).  
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF  
 CC INTERLEUKINS.  
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND  
 CC PROBABLY ALSO THE IL-13 RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED  
 CC SEVERE COMBINED IMMUNODEFICIENCY.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: 004361; AAC048403.1;  
 CC DR HSSP: P31785; ILLN.  
 DR PRAM: P00041; fn3; 1.  
 DR PROSITE: PS00241; RECEPTOR\_CYTOKINES\_1; 1.  
 DR PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; FALSE\_NEG.  
 KW Receptor; Transmembrane; Glycoprotein; signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 373  
 FT DOMAIN 23 373  
 FT TRANSMEM 262 283  
 FT DOMAIN 284 373  
 FT DISULFID 62 72  
 FT DISULFID 102 115  
 FT CARBOHYD 24 24  
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 FT CARBOHYD 249 249  
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Query Match 8.9%; Score 207; DB 1; Length 373;  
 Best Local Similarity 25.1%; Pred. No. 7.3e-09;  
 Matches 76; Conservative 52; Mismatches 131; Indels 44; Gaps 14;

CC 88 VPLNERICLOVGSOCSTNESEKRSILVEKICSPEDDPESATVLOCIMHNSYKCSWLP 147  
 DB 21 VGLNSTVPMRG-----NEDITPDLATPSETLSVSLPEVOCFVFNVEYNNCTGN 75  
 CC 148 PGRNTSPDITVYLYWHRSL-EKIHOCEN-IPREGQYGCSDLVKVDSSFECHSVQI 204  
 DB 76 SSSPFR-TNLLHYWKKNNDKVOEGCHYLFKRYTAGCW--LQKEIHLIEFFVQOL 132  
 CC 205 MYMDNAGKIRPSNIYPLSRVPPPHIKNLSFN--DDLYQWENPQNFISRCLEFE 261  
 DB 133 --DPPRPRQOSTOKRLQNLVTPMAP--ENLTLNLSQGLSMNS--RLDHCLEHV 186  
 CC 262 VEYNSQTEHNVFYQEAKECENPEFERNVENTSCMVGCVLPDLINTVIRKYNKLCY 321  
 DB 187 VOYRSDMRNT-----ECSVDRHNSLSLPVDGQKFFRYFRVRSRNPICG 232  
 CC 322 EDDKLSMNSOEMSICKR--KNSTLYITMLLIPYIVAGAILVL--LYLKRILTIIFP 376  
 DB 233 SAQR-MSESHPIHMGSNSTSKENPLFASEAVLPLGSMGLISLICYWYLER-----SIP 287  
 CC 377 PIP 379  
 DB 288 RIF 290

RESULT 8  
 CTRG\_MOUSE  
 ID CTRG\_MOUSE STANDARD; PRT: 369 AA.  
 AC P34902;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).  
 GN IL2RG.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 33277575.  
 RA KUMAKI S., KONDO M., TAKESHITA T., ASAO H., NAKAMURA M., SUGAMURA K.;

Query Match	Similarity	Score	DB 1	Length
Best Local Similarity	24.0%	205.5	DB 1	369
Matches	76	Conservative	63	Mismatches 121; Indels 57; Gaps 16;
Query	103	STPSEKPSILYKISIPEDGDEANVLEIQIMNLSYMGCSMLPGNTSPD---	TNT	159
Db	31	SANEDIKADLITSTAPHLSPATLPLEVOCEVENIEMNCTW---NSSEPOATINT	86	
Query	160	LYYHRSLEKIHOCENIFREGOFGCSEDTLVKNSSEFOHSVQ-----INVKDNAGKI	213	
Db	87	LHYRKYVD-----NNTFOECHYLFNSKIT--SSCQIKNEDIQLYQTFVQLODPQRQ	139	
Query	214	KPSFIVPLTSVNPDPPIKNSLHFN--DDLYQWENPWFISCLFEYEVNNSQTE	270	
Db	140	RYVYKMLQNLVIRAP--ENLITSLNSESQLEDRKMS-RIKIKERCLQYLVQYRSNDR	196	
Query	271	TNNVYVOEAKCENPEFRNVENTSCFMPGVGLPPTLN--TVRIYKTKLCEYEDKLS	328	
Db	197	SVT-----ELIYNHERFSIPSV--DELKRYTRVRSRNPICGSSQ--WS	239	
Query	329	NWSQMSIGK--KRNSTLYTMLLIVPYVAGAILVLL--YKRLKIIFPPIPDG	382	
Db	240	KMSQVHMGSHTVEENPSLFALEAVLIPVGTGLITLIFYCMLERM-----PPI-P	293	
Query	383	KIKFEMGDQNDLTHW	399	
Db	294	KNLELVTEYQGNFSAW	310	
RESULT	9			
CYRG_HUMAN	STANDARD:	PRT:	369 AA.	
ID	CYRG_HUMAN	STANDARD:	PRT:	369 AA.
Accession	P31785			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	CYOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (p64) (CD132 ANTIGEN).			
GN	IL2RG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
NC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
PN	[1]			
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.			
FX	MEDLINE: 92335883.			
FA	TAKEISHITA T., ASAO H., OHTANI K., ISHII N., KURAKI S., TANAKA N.,			
RT	"Cloning of the gamma chain of the human IL-2 receptor."			
FM	Science 257:379-382(1992).			
FM	[3]			
RZ	SEQUENCE FROM N.A.			
RZ	TISSUE-LIVER.			
RZ	MEDLINE: 93293887.			
FA	NOUCHI M., ADESTEIN S., CAO X., LEONARD W.J.;			
RT	"Characterization of the human interleukin-2 receptor gamma chain			

RT gene.";  
 RL J. Biol. Chem. 268:13601-13608(1993).  
 [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.  
 RX MEDLINE: 94004847.  
 RA PUCK J.M., DESCHERES S.M., PORTER J.C., DUTRA A.S., BROWN C.J.,  
 RA WILLARD H., HENTHORN P.S.;  
 RT "The interleukin-2 receptor gamma chain maps to xq13.1 and is mutated  
 in X-linked severe combined immunodeficiency. SCIDX1.";  
 RL Hum. Mol. Genet. 2:1099-1104(1993).  
 [4]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE: 94090315.  
 RA KONO M., TAKESHITA T., ISHII N., NAKAMURA M., WATANABE S.,  
 RA ARAI K.-I., SUGAMURA K.;  
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between  
 receptors for IL-2 and IL-4.";  
 RL Science 262:1874-1877(1993).  
 [5]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE: 94090317.  
 RA RUSSELL S.M., KEGAN A.D., HARADA N., NAKAMURA Y., NOGUCHI M.,  
 RA LELAND P., FRIEDMAN M.C., MIYAJIMA A., PURI R.K., PAUL W.E.,  
 RA LEONARD W.J.;  
 RT "Interleukin-2 receptor gamma chain: a functional component of the  
 interleukin-4 receptor.";  
 RL Science 262:1880-1883(1993).  
 [6]  
 RP IDENTIFICATION AS A IL-7R SUBUNIT.  
 RX MEDLINE: 94090316.  
 RA NOGUCHI M., NAKAMURA Y., RUSSELL S.M., ZIEGLER S.F., TSANG M., CHAO X.,  
 RA LEONARD W.J.;  
 RT "Interleukin-2 receptor gamma chain: a functional component of the  
 interleukin-7 receptor.";  
 RL Science 262:1877-1880(1993).  
 [7]  
 RP 3D-STRUCTURE MODELING OF 57-248.  
 RX MEDLINE: 95111955.  
 RA BAMBOURGH P., HEDGECOCK C.J., RICHARDS W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 modelling.";  
 RL Structure 2:839-851(1994).  
 [8]  
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.  
 RX MEDLINE: 94130970.  
 RA DISANTO J.P., DAUTRY-VARSAT A., CERTAIN S., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked  
 severe combined immunodeficiency disease result in the loss of  
 high-affinity IL-2 receptor binding.";  
 RL Eur. J. Immunol. 24:475-479(1994).  
 [9]  
 RP VARIANT XSCID LYS-68.  
 RX MEDLINE: 94375038.  
 RA MARLEWICZ S., SUBTIL A., DAUTRY-VARSAT A., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Detection of three nonsense mutations and one missense mutation in  
 the interleukin-2 receptor gamma chain gene in SCIDX1 that  
 differentially affect the mRNA processing.";  
 RL Genomics 21:291-293(1994).  
 [10]  
 RP VARIANT XSCID HIS-162.  
 RX MEDLINE: 94300093.  
 RA ISHII N., ASAO H., KIMURA Y., TAKESHITA T., NAKAMURA M., TSUCHIYA S.,  
 RA KONNO T., MAEDA M., UCHIYAMA T., SUGAMURA K.;  
 RT "Impairment of ligand binding and growth signaling of mutant IL-2  
 receptor gamma-chains in patients with X-linked severe combined  
 immunodeficiency.";  
 RL J. Immunol. 153:1310-1317(1994).  
 [11]  
 RP VARIANT XSCID ASN-39.  
 RX MEDLINE: 95023932.  
 RA DISANTO J.P., RIEUX-LAUCAT F., DAUTRY-VARSAT A., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X  
 chromosome-linked severe combined immunodeficiency with peripheral T  
 cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).  
 [12]  
 RP VARIANTS XSCID CYS-226 AND HIS-226.  
 RX MEDLINE: 95397841.  
 RA PEPPER A.E., BUCKLEY R.H., SMALL T.N., PUCK J.M.;  
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain  
 gene causing human X-linked severe combined immunodeficiency.";  
 RL Am. J. Hum. Genet. 57:564-571(1995).  
 [13]  
 RP VARIANT XSCID SER-183.  
 RX MEDLINE: 96013903.  
 RA CLARK P.A., LESTER T., GENET S., JONES A.M., HENDRIKS R.,  
 RA LEVINSKY R.L., KINNON C.;  
 RT "Screening for mutations causing X-linked severe combined  
 immunodeficiency in the IL-2R gamma chain gene by single-strand  
 conformation polymorphism analysis.";  
 RL Hum. Genet. 96:427-432(1995).  
 [14]  
 RP VARIANT XSCID GLN-TRP INS-237.  
 RX MEDLINE: 95164726.  
 RA PUCK J.M., PEPPER A.E., BEDARD P.-M., LAFRANCOISE R.;  
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor  
 gamma-chain mutation causing X-linked severe combined  
 immunodeficiency.";  
 RL J. Clin. Invest. 95:895-899(1995).  
 [15]  
 RP VARIANT XSCID GLN-271.  
 RX MEDLINE: 95190013.  
 RA SCHWALSTIG F.C., LEONARD W.J., NOGUCHI M., BERG M., RUDLOFF H.E.,  
 RA DENNEY R.M., DAVE S.K., BROOKS E.G., GOLDMAN A.S.;  
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a  
 moderate form of X-linked combined immunodeficiency.";  
 RL J. Clin. Invest. 95:1169-1173(1995).  
 [16]  
 RP VARIANT XSCID ARG-115.  
 RX MEDLINE: 97042245.  
 RA STEPHAN V., WAHN V., LE DEIST F., DIRKSEN U., BROKER B.,  
 RA MULLER-FLECKENSTEIN I., HORNEFF G., SCHOTEN H., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Atypical X-linked severe combined immunodeficiency due to possible  
 spontaneous reversion of the genetic defect in T cells.";  
 RL New Engl. J. Med. 335:1563-1567(1996).  
 [17]  
 RP VARIANT XSCID GLN-285.  
 RX MEDLINE: 97295088.  
 RA JONES A.M., CLARK P.A., KATZ F., GENET S., MCMAHON C., ALTERMAN L.,  
 RA CANT A., KINNON C.;  
 RT "B-cell-negative severe combined immunodeficiency associated with a  
 common gamma chain mutation.";  
 RL Hum. Genet. 99:677-680(1997).  
 [18]  
 RP VARIANT XSCID CYS-222.  
 RX MEDLINE: 98064061.  
 RA SHARFE N., SHAHAR M., ROIFMAN C.M.;  
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus  
 morphology.";  
 RL J. Clin. Invest. 100:3036-3043(1997).  
 [19]  
 RP FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF  
 INTERLEUKINS.  
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND  
 IL-13 RECEPTORS.  
 CC -1- PROBABLY ALSO THE IL-13 RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED  
 IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE  
 OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide cd132 entry;  
 CC -1- WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".





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OY 236 LSFHNDLYVOMENPONTISR-----CLFEYEVENNSQTEHNVFYVOAKCENPEFERNV 291
DB 343 PINRRPYLMLTSPPLADVRSGMLTLDYELRLKPEGEWEIVFGQ-QTOYKMSLN- 401
OY 292 ENTSCFMPGVLPDLNTVIRIRYKTKLCYEDDKLMSNMSQSKKRNSTLYITMLLI 351
DB 401 -----PGKKYIIOIHCKP-----DHGGSWSESSSENYEIPNDFVKDMIVMI 443
OY 352 VPYVAGATIVLL---LYLKRLLIIF--PRIPDP 381
DB 444 VLGVLSLLICLMSWTMLNGYMTIFILPVPGP 478

RESULT 11
PRLR_CHICK STANDARD: PRT: 831 AA.
AC 004594.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LECHORN; TISSUE-KIDNEY;
RX MEDLINE; 93075121.
RA TANAKA M., MAEDA K., OKUBO T., MAKASHIMA K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
the cDNA sequence."
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL: D13154; BAA02439.1; -
DR PIR: JQ1655; JQ1655.
DR HSP: P16471; 1BP3.
DR PFAM: PF00041; fn3. 4.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 438
FT DOMAIN 24 438 PROLACTIN RECEPTOR.
FT TRANSMEM 439 459 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 460 831 POTENTIAL.
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 123 122 FIBRONECTIN TYPE-III.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 POTENTIAL.
FT CARBOHYD 91 91 POTENTIAL.
FT CARBOHYD 100 100 POTENTIAL.
FT CARBOHYD 112 112 POTENTIAL.
FT CARBOHYD 132 132 POTENTIAL.
FT CARBOHYD 262 262 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.

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FT CARBOHYD 315 315 POTENTIAL.
FT CARBOHYD 335 335 POTENTIAL.
SQ SEQUENCE 831 AA; 94102 MW; 8977BF07 CRC32;

Query Match
Best Local Similarity 23.1%; Score 197.5; DB 1; Length 831;
Matches 91; Conservative 59; Mismatches 159; Indels 85; Gaps 19;

OY 32 OP--PTNINSVENICV--TWT-WNPP--EGASSNSLSWFFSHFGKODKKIADERR 84
DB 126 QGSPV-NLTETKRSANIMYLAKMSPLADASSN---HLHY---ELRIPEERE 176
OY 85 SIEVPLNERICQVGSOCSTNE-----SEKPSILVERCISP 121
DB 177 EWEI-----ISVQTOQCINRLNMGKRYVQRCITLDPEGSEWSESRHILIPSGSP 231
OY 122 EGDPSAVTELOCIMHNLSYMKCSWLPGRNTSPDITNLYWHSLEKIHOCENIFREGO 181
DB 232 E-----KPTIIRKRPKEKETFCKMKPGIDGHPNITLYLSKEGEQVYECFD-YRTAG 285
OY 182 YFGCFDLTKVNDSEFGHSVQIMKDNAGKIKPSFNIVPLTSRYKPPDP-----HINKL 236
DB 286 PMSCTFD--KHTSPWITYNITVRATNENGSSDPHYVDVITYVOPDPVAVTLELKP 343
OY 237 SFHNDLYVOMENPONTISR-----CLFEYEVENNSQTEHNVFYVOAKCENPEFERNV 292
DB 344 INRRPYLMLTSPPLADVRSGMLTLDYELRLKPEGEWEIVFGQ-QTOYKMSLN-- 401
OY 293 NTSCFMPGVLPDLNTVIRIRYKTKLCYEDDKLMSNMSQSKKRNSTLYITMLLI 352
DB 401 -----PGKKYIIOIHCKP-----DHGGSWSESSSENYEIPNDFVKDMIVMI 444
OY 353 VPYVAGATIVLL---LYLKRLLIIF--PRIPDP 381
DB 445 VLGVLSLLICLMSWTMLNGYMTIFILPVPGP 478

RESULT 12
CYRG_BOVIN STANDARD: PRT: 379 AA.
AC 095118.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
(INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovine; Bos.
FT [1]
FT SEQUENCE FROM N.A.
FT MEDLINE; 96268473.
RA YOO J., STONE R.T., SOLINAS-TOLODO S., FRIES R., BEATTIE C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
gamma gene."
RL DNA Cell Biol. 15:453-459(1996).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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FT CARBOHYD 99 99
FT CARBOHYD 127 127
FT VARSPLIC 131 150
FT VARSPLIC 151 610
FT VARSPLIC 281 310
FT VARSPLIC 311 610
FT VARSPLIC 342 539
FT CONFLICT 236 236
FT CONFLICT 345 345
FT CONFLICT 465 465
FT CONFLICT 466 466
FT CONFLICT 469 469
FT CONFLICT 541 541
FT CONFLICT 555 555
SQ SEQUENCE 610 AA: 68599 MW: C579BC43 CRC32:

POTENTIAL.
EYKOLKDKKTYLWVKSPPPT -> DYRWVSCHEALPKSA
KIN (IN SHORT FORM).
MISSING (IN SHORT FORM).
KKSSELLALCCODEPPPSDCELDLVEFL ->
TGPSKYVDLYALPGFGFKLDNAGELDY (IN
MEDIUM FORM).
MISSING (IN MEDIUM FORM).
MISSING (IN FORM N22).
V -> A (IN REF. 2).
G -> V (IN REF. 2).
E -> K (IN REF. 1).
Q -> E (IN REF. 2).
A -> G (IN REF. 2).
T -> M (IN REF. 1).
Q -> K (IN REF. 2).

Query Match
Best Local Similarity 23.7%; Score 189; DB 1; Length 610;
Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KSLIVERKISPEGDPESAVTELQCIWHLNLSYKCSWLPGRNTSPDNTYLYWHSLE 168
DB 25 KPEI--HKCRSP--DKET-----FTCMWNPBGTDGGLPTNYSLEKEGK 65

QY 169 KIHOCENIREQYFGCSFDLTWKVDSFEQHSVOIWKDNAGKIKPSFNIVPLTSRYK 228
DB 66 TTYECDDYVTSGN--SCFP--SKQYTSIMKITYITVATNQMSSSSDPLVDVYTVI 122

QY 229 DPP-----HIKLSFHNDDLYQWENPQNFISR---CLFEYEVNNSQTEHNFYVOE 279
DB 123 EPPRNLJLEVKQKDKKTYLWVKSPPITLDVKTGFTMEYELRLKPEKEEHEIHF-- 180

QY 280 ACCENEFERNENVENTSCFVPGVLPDLTVIRIVKTNKLCYEDDKLWNSQEMSIGK 339
DB 180 -----TGHOTQFVFYFDLYPGOKYLVQTR-----CKPDHGYWRSQSSSEVEMP 222

QY 340 RNSTLYITMLIVPVAGAILVLLYLKRLK-----IIFPPIPP 381
DB 223 NDTLADITVITVAILSAVICLIWMAVALKGYSMATCIPFPVGP 269

RESULT 14
PRLR_BOVIN STANDARD: PRT; 581 AA.
AC Q28172;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE; 93246019.
RA SCOTT P., KESSLER M.A., SCHULER L.A.;
RT "Molecular cloning of the bovine prolactin receptor and distribution
RT of prolactin and growth hormone receptor transcripts in fetal and
RT utero-placental tissues."
RL Mol. Cell. Endocrinol. 89:47-56(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC or send an email to license@sib-sib.ch).
CC -----
CC SML: 102549; AA51417.1;
CC HSSP; P14787; 1AN3;
DR PPM, PF00041; 1N3; 2.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW Receptor; Transmembrane; Glycoprotein; signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFD 36 46
FT DISULFD 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
SQ SEQUENCE 581 AA; 65153 MW; COECAA02 CRC32;

Query Match
Best Local Similarity 24.3%; Score 186; DB 1; Length 581;
Matches 80; Conservative 44; Mismatches 115; Indels 90; Gaps 16;

QY 108 KPSILVERKISPEGDPESAVTELQCIWHLNLSYKCSWLPGRNTSPDNTYLYWHSLE 167
DB 29 EKPKLY--KCRSPGK-----ETTCWNEPBGADGGLPTNITLTHKGE 69

QY 168 KIHOCENIREQYFGCSFDLTWKVDSFEQHSVOIWKDNAGKIKPSFNIVPLTSRYK 227
DB 70 TLHPCPD-YKNGGPNSCF--SKKHTSIMKMYVITVANINQMGISSDPLVHTYIYE 126

QY 228 DPPPHIKNLSF--HNDD---LYQWENPQNFISRCLFEYEVNNSQTEHNFYVOE 270
DB 127 PPP--ANLTLEKHPEDRKPYLWIKWSPPTWTVKSGMFI---IYELRLKPEKATDWE 181

QY 271 THNFFVVOEAKCENPEERNVENTSCFVPGVLPDLTVIRIVKTNKLCYEDDKLWNSQ 330
DB 182 THFTLKQOLKFN-----LYPGOKYLVQIR-----CKPDHGYWSEW 218

QY 331 SQEMSIGKRNSTLYITMLIVPVAGAILVLLYLKRLK-----IIFPPIPPGKIF 385
DB 219 SPESLIQIPNDPVDTSIMWIFVAILSAVICLIWMAVALKGYSMATCIPFPVGP-KI- 277

QY 386 KEMFGQNDTILMKKKYDIY--EKQTKEE 412
DB 277 -----KGFVHLEKGSSE 291

RESULT 15
PRLR_RABIT STANDARD: PRT; 616 AA.
AC P14787;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY GLAND;
RX MEDLINE; 89184578.

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Search completed: January 20, 2000, 06:19:57  
 CPU time: 94 sec

RA EDERY M., JOLICOEUR C., LEVI-MEXRUBIS C., DUSANTER-FOUR I.,  
 RA PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DIANE J.,  
 RT Identification and sequence analysis of a second form of prolactin  
 RT receptor by molecular cloning of complementary DNA from rabbit  
 RT mammary gland.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).  
 RN [2]  
 RP 3D-STRUCTURE MODELING OF 30-228.  
 RX MEDLINE: 97248733.  
 RA HALABY D., THOREAU E., DIANE J., MORON J.P.:  
 RT "Homology modeling of rabbit prolactin hormone complexed with its  
 RT receptor.";  
 RL Proteins 27:459-468(1997).  
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
 CC PROLACTIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@isb-slb.ch](mailto:license@isb-slb.ch)).  
 CC  
 CC EMBL: J04510; AAA1457.1: -  
 DR PIR: A30304; A30304.  
 DR PDB: 1AN3; 03-DEC-97.  
 DR PFAM: PF00041; fn3: 2.  
 DR PROSITE: PS00241; RECEPTOR\_CYTOKINES\_1; 1.  
 DR PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.  
 FT SIGNAL 1 24  
 FT CHAIN 25 616  
 FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 235 258 POTENTIAL.  
 FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 124 227 FIBRONECTIN TYPE-III.  
 FT DOMAIN 124 227 FIBRONECTIN TYPE-III.  
 FT DISULFID 36 46 BY SIMILARITY.  
 FT DISULFID 75 86 BY SIMILARITY.  
 FT CARBOHYD 59 59 POTENTIAL.  
 FT CARBOHYD 104 104 POTENTIAL.  
 FT CARBOHYD 132 132 POTENTIAL.  
 SQ SEQUENCE 616 AA; 68840 MW; FB6170B1 CRC32;

Query Match 8.0%; Score 185; DB 1; Length 616;  
 Best Local Similarity 27.3%; Pred. No. 6.9e-07;  
 Matches 80; Conservative 40; Mismatches 105; Indels 68; Gaps 17;

OY 109 KPSILVEKCI SPPEGDPESAVTELCIWNLSYMKCSWLPGRNTSPDNTLYLWHRSL 168  
 DB 30 KPRIFF-KCRSPKX-----ETFTCMWRGADGGLPTNTLYL-HKEGE 69  
 OY 169 KI-HOCENIFREGQYFGCSFDLTKVDSFEQSVQIMVADNKGKIKPSFNIVPLTSRK 227  
 DB 70 TIHCECPD-YKTGGPNSCYF-SKHTISWTIYIIIVNATNMGSSVSDPRYVDVYIYE 126  
 OY 228 PDPPHKNLSF---HNDD---LYVOMENQNTISR---CLFYEEV---NNSQETHN 273  
 DB 127 PDPP--VNLTLEVKHPEDRKPYLWVKMLPPTLYDVNSGWLTLQYETRLKPKAEWETH- 184  
 OY 274 VEVYQAKCENPEERFENVENTSCFVWPGVLPDLNTVRIKTKNKLCYEDDKLMSNWSQ 333  
 DB 184 -FAGQQTQ-----FKILSLPGQKYLQVR-----CKPDHGFMSVMSPE 221  
 OY 334 MSIGKRNSTLY-ITMLLYPVI--VAGATIVLLYLKRLKI--IFPPIPD 381  
 DB 222 SSIOINDEFTWITWIFAVAVLSTIICLIIMWAVALKGYSMTCIFPPVGP 274

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QY 361 IYLLLYLKLKLIIPPPIDPGKIFKEMFGDONDDTLHMKKYDIYEKOTKEEDSVLLIE 420  
 DB 361 IYLLLYLKLKLIIPPPIDPGKIFKEMFGDONDDTLHMKKYDIYEKOTKEEDSVLLIE 420  
 QY 421 NUKRASQ 427  
 DB 421 NUKRASQ 427

## RESULT 2

097597 PRELIMINARY: PRT: 349 AA.

AC 097597  
 DT 01-MAY-1999 (TRENBLREL. 10, Created)  
 DT 01-MAY-1999 (TRENBLREL. 10, last sequence update)  
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
 OC Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TRIGONA W.L., HIRANO A., BROWN W.C., ESTES D.M.;  
 RT "Biological Activities of Interleukin-13 on bovine lymphocytes:  
 RT Implications for signaling through IL-13R $\alpha$ 1."  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF074402; AAC98147.1; .  
 KW Receptor.  
 FT NON-TER  
 FT NON-TER  
 SQ SEQUENCE 349 AA: 39644 MW: AB48972 CRC32;

Query Match 69.3%; Score 1610; DB 6; Length 349;

Best Local Similarity 84.5%; Pred. No. 3.9e-133; Matches 295; Conservative 17; Mismatches 37; Indels 0; Gaps 0;

QY 35 VTNLSVSENICTVITWNPPEGASNCSLWYFSHFGDKODKRIAPETRSIEVPLNERI 94  
 DB 1 VTNLSVSENICTVITWNPPEGASNCSLWYFSHFGDKODKRIAPETRSIEVPLNERI 60  
 QY 95 CLQVSOQSTNSEKPSILVEKCIPEEDPSAVTELOCITMHNLSYKCSWLPGRNISP 154  
 DB 61 CLQVSOQSTNSEKPSILVEKCIPEEDPSAVTELOCITMHNLSYKCSWLPGRNISP 120  
 QY 155 DNTYLLTYWHRSLERKIHOCENIFREGQVGCSEFDLTKVDSSEFQHSVQIMKDNAGKIS 214  
 DB 121 DNTYLLTYWHRSLERKIHOCENIFREGQVGCSEFDLTKVDSSEFQHSVQIMKDNAGKIS 180  
 QY 215 PSFNIVPLTSRVKPPPHIKNLFSHNDLYVQWENPQNFISRCLEFEVEVNNSTETNAV 274  
 DB 181 PSFNIVPLTSRVKPPPHIKNLFSHNDLYVQWENPQNFISRCLEFEVEVNNSTETNAV 240  
 QY 275 FYVOAKCENPEFERNVENTSCFMPGVLPDLNLYVRIKYNKLCYEDDKLMSWSQAM 334  
 DB 241 FYVEAKCENPEFERNVENTSCFMPGVLPDLNLYVRIKYNKLCYEDDKLMSWSQAM 300  
 QY 335 SIGKRNSLTITMLLIYVAGAIYVLLYKRLKIIFPPIDPGK 383  
 DB 301 SIGKRNSLTITMLLIYVAGAIYVLLYKRLKIIFPPIDPGK 349

RESULT 3  
 ID 014633 PRELIMINARY: PRT: 420 AA.  
 AC 014633  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, last sequence update)  
 DE INTERLEUKIN-5 RECEPTOR PRECURSOR.  
 GN HSTL5R.  
 OS Homo sapiens (Human);

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD.  
 RX MEDLINE: 92121815.  
 RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 RT receptor."  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X61176; CAA43483.1; .  
 FT SIGNAL  
 FT CHAIN  
 SQ SEQUENCE 420 AA: 47670 MW: 247AB980 CRC32;

Query Match 12.7%; Score 294.5; DB 4; Length 420;

Best Local Similarity 24.8%; Pred. No. 6e-18; Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

QY 33 PVTNLSVSENICTVITWNPPEGASNCSLWYFSHFGDKODKRIAPETRSIEVPLN 91  
 DB 32 PVTNLSVSENICTVITWNPPEGASNCSLWYFSHFGDKODKRIAPETRSIEVPLN 82  
 QY 92 ERICLOV-----GSQSTNSEKPSILVEKCI-----PPEGDPESAVTELOCIMHNL--- 140  
 DB 83 ERICLOV-----GSQSTNSEKPSILVEKCI-----PPEGDPESAVTELOCIMHNL--- 142  
 QY 140 -----SY--MKCSWLPGRNISPDLNLYVWHRSLERKIHOCENIFRE--GQYEGCSDDL 189  
 DB 143 YSRLRSYGVSLHCTVLVGTDAPEDTQYFLYRYSWTE--ECQESKDTLRNINACWPPR 200  
 QY 130 TKVDSSEFQHSVQIMKDNAGKISFNIVPLTSRVKPPPHIKNLFSHNDLYVQWEN 249  
 DB 201 TKVDSSEFQHSVQIMKDNAGKISFNIVPLTSRVKPPPHIKNLFSHNDLYVQWEN 260  
 QY 250 PON-FISRCLEFEVEVNNSTETNAVYVOAKCENPEFERNVENTSCFMPGVLPDLN 308  
 DB 261 PVSAPRIPCDEVEYVHNTNG-----YLOIEKLMNTAFISIDLSY----- 305  
 QY 309 TYRTRVKNKLCYEDDKLMSWSQAMSIGKRNSLTITMLLIYVAGAIYVLLYK 368  
 DB 305 DVQVAAVSSMCRKENG-LMSEMSQPIYVGNDEHKLPLREMFIVIMATICTILLISLICK 363  
 QY 369 --RLKIIFPPIDPGKIFKEMFGDONDDTLHMKKYDIYEKOTKEEDSVVL 418  
 DB 364 ICHLWIKIFPPIDPGKIFKEMFGDONDDTLHMKKYDIYEKOTKEEDSVVL 404

RESULT 4  
 ID 088786 PRELIMINARY: PRT: 383 AA.  
 AC 088786  
 DT 01-NOV-1998 (TRENBLREL. 08, Created)  
 DT 01-NOV-1998 (TRENBLREL. 08, last sequence update)  
 DE IL-13 RECEPTOR ALPHA 2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C3H/HEJ; TISSUE-THYMUS.  
 RX MEDLINE: 98391042.  
 RA DONALDSON D.D., WHITTEN M.J., FITZ L., NEBBEN T.Y., FINNERTY H.,  
 RA HENDERSON S.L., O'HARA R.M., JR., BEIER D.R., TURNER K.J., WOOD C.R.,  
 RA COLLINS M.;  
 RT "The murine IL-13 receptor alpha 2: molecular cloning,  
 RT characterization, and comparison with murine IL-13 receptor alpha  
 RT 1."  
 RL J. Immunol. 161:2317-2324(1998).  
 DR EMBL: U65747; AAC33240.1; .

SEQUENCE 383 AA: 44483 MW: 5EAEF3E3 CRC32:

Query Match 12.4%; Score 287.5; DB 11; Length 383;

Best Local Similarity 25.6%; Pred. No. 2.2e-17; Indels 49; Gaps 14;

Matches 89; Conservative 54; Mismatches 156; Indels 49; Gaps 14;

52 WNP-----EGASSNCSLWYFSHFGDKODKKAPEPRRSIEVPLNE---RIGLQVGSQ 101  
 47 WKRPVIEKFGCTLEVELEKRYVDSMTITRNLIYDGDILNKIGIKRTLSER 106  
 102 CSTNESEKPSILVEKIS--PEGDPSAVTELQCIWHLNLSYKCSWLPGRNTSPDITVL 160  
 107 C-INGSEVQSPWIEASGIDSESLFKIDMKCIYNNQIYLVCSMKPKRTYSDIYTM 165  
 161 YVHRLERKHOCENIFR--EGYFGSGFDLTKYKDSFEQSHVQIWKDAGIKPSPNI 219  
 166 FEWYEGIDHALQCADYLQHDEKNVCK--LSNIDSSDYKFFICVNGSSKLEPIRSSYTV 223  
 220 VPLTSRKVPPPIKINLSFEND-DLYVQWENPQNEI-SRCLFEVEVNSQTEHNFYV 277  
 224 FOLQNIYKPLPPEFLHISVNSIDIRKAKSTPGPIPPKCTTEIYVIREDISVESATDK 283  
 278 QEAKCENPEFERVENTSCFMPGVLPDLTVIRKYNKLCYEDDKLMSNSQEMS-- 336  
 284 NDKLKR--RANESEDLCPFY-----RCKVNIYC-ADDGIMSEWSEECWE 326  
 336 --IGKRNSTLYITMLIVPIYAGAIYVLLYLRKIKIIFPIPD 381  
 327 GYTPDSK-----IIFIVVCFEFLILLCL-----YKEKEPDP 363

RESULT 5

Q14631 PRELIMINARY: PRT: 396 AA.

AC Q14631: 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.  
 GN HS15SR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RX MEDLINE: 92121815.  
 RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 receptor."  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X61177; CAA43484.1; --.  
 KW SIGNAL.  
 FT SIGNAL. 1 20 POTENTIAL.  
 FT CHAIN 21 396 INTERLEUKIN-5 RECEPTOR TYPE 2.  
 SO SEQUENCE 396 AA: 44998 MW: 85F8F684 CRC32:

Query Match 12.2%; Score 282.5; DB 4; Length 396;

Best Local Similarity 24.4%; Pred. No. 6.3e-17; Indels 65; Gaps 16;

Matches 98; Conservative 64; Mismatches 174; Indels 65; Gaps 16;

33 PPTNLSYVENICTYIWTNP--PEGASSNCSLWYFSHFGDKODKKAPEPRRSIEVPLN 91  
 32 PVP-NTTITKTAQVLLQWKPMPDQQRNVNLEY-----OVKINAPK-EDDYETIRIT 82  
 92 ERICLOV-----GSQSTNESEKPSILVEKIS--PEGDPSAVTELQCIWHLN--- 140  
 83 ESMCVIILHKGFSASVRTIIONDHSILASSWABALHAPGSGTISVNLCTTTEDN 142  
 140 ---SY---MKCSWLPGRNTSPDITNLYVHRSLEKIHOCENIFRE--GYFGSGFDL 189

143 YSRIRCYVSLHCTWLVGTADAPEDTQFLYRYGSWTE--ECOYSKDTLGRNIACMPFR 200  
 190 TKVADS-TEBOHSVQIWKDAGIKRPSFNIPLTSRKVPPPIKINLSFHNDDLYQWEN 249  
 201 TFLISGRDMLAVLVGSSKSHAIRFPDOLFALHAIQDINPLNTVAELIGTSLQWEX 260  
 250 PON-FISRLCFEVEVNSQTEHNFYVQOAKCENPEFERVENTSCFMPGVLPDITLN 308  
 261 PVSAFPHCEDEYVKIKHNRNG-----YLQELKMLNAFISIIDLSKY----- 305  
 309 TVARVYKTKLYCEDDKLMSNSQEMSIGKRNSTLYITMLIVPIYVACIIVLLYLR 368  
 305 DVQVRAVSSMCRRAC-LWSEQSPPIYVGNDEKPLREMFVIVMATIGIFILLISLICK 363  
 369 --RLYTIIPPIPDGKIFKEMFGQNDOTLHWKTDIYK 407  
 364 ICHLWIKLEPPIDAPKSNIKDLFVTTN-----YEK 393

RESULT 6

Q920K4 PRELIMINARY: PRT: 415 AA.

AC Q920K4: 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.  
 GN GPIL-FRA.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MORRIS T.E.;  
 RT "Cloning and Characterization of the Guinea Pig Interleukin-5  
 Receptor alpha cDNA."  
 RX Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.  
 LR EMBL: U55215; AAD09361.1; --.  
 KY SIGNAL; Receptor.  
 FT SIGNAL. 1 17 POTENTIAL.  
 FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA.  
 SO SEQUENCE 415 AA: 46913 MW: 99B8C82 CRC32:

Query Match 12.0%; Score 279.5; DB 11; Length 415;

Best Local Similarity 23.7%; Pred. No. 1.2e-16; Indels 71; Gaps 17;

Matches 100; Conservative 65; Mismatches 186; Indels 71; Gaps 17;

29 TETOP-----PVTNLSYVENICTYIWTNP--PEGASSNCSLWYFSHFGDKODKKA 80  
 17 TDTLPKPKFLLPINFTIKYGLAVLVQWEPNPNQGNKVNLANHYINTPQEDDY-- 75  
 81 ETRFS--IEVPLNERICLQVGSQSTNESEKPSILVEKISPEGDPSAVTELQCI-- 136  
 75 ETRFSGS-CEETLHOGVSAVRTIILHGHSLASSWVSAEHKAPSPGSPSTISVNLCTTN 134  
 136 ---WENL-SY---MKCSWLPGRNTSPDITNLYVHRSLEKIHOCENIFRE--G 180  
 135 TAASNTNLSKSEVSLHCTWLVGTADAPEDTQFLYRYGSPW-----TECOYSKDTLS 188  
 181 QYFGSFDLTKYVDSFEQSHVQIYKDNAGIKRPSFNIPLTSRKVPPPIKINLSFHN 240  
 189 RNACWCFEPTIFHSKARDLAVHNGSSSHATIKFPDOLFQVADIDQPPMPDYATETGS 248  
 241 DDIYQWENPON-FISRLCFEVEVNSQTEHNFYVQOAKCENPEFERVENTSCFMPV 299  
 249 SRLSIGQKPVSAFPHCEYEVKICHTKD-----YQVEKTTNAFSTIDGVSKY-- 301  
 300 PGVLPDLTVIRVRYKTNKLYCEDDKLMSNSQEMSIGKRNSTLYITMLIVPIYVACA 359  
 361 ---SIOVRAVSSPHC--RAMGLMSKWSQPYVVGKKRP--TAGWFLITLITAVLGF 348  
 360 IIVLLYLRKIKI--IIPPIPDGKIFKEMFGQNDOTLHWKTDIYKQTEETDSV 416

Db 349 ILLIFFLCRIYHMTKMPVPAPKSTFKDLIMTNT-----CEKAGSSETEIE 397  
 Oy 417 VL 418  
 Db 398 VI 399

## RESULT 7

015469 PRELIMINARY: PRT: 333 AA.

AC 015469  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.  
 GN HSIL5R4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD:  
 RX MEDLINE: 92121815.  
 RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 receptor";  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X62156; CAA44081.1; .  
 KW Signal.  
 FT SIGNAL. 1 20 POTENTIAL.  
 FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.  
 SQ SEQUENCE 333 AA: 37722 MW; E86A7792 CRC32;

## Query Match

Best local similarity 9.5%; Score 229; DB 4; Length 333;  
 Matches 81; Conservative 52; Mismatches 145; Indels 52; Gaps 14;

Oy 33 PPTVNLVSVENLCVITWMPN-PEGASSNCSLWTFSHRGDKQKRIAPETRSIEVPLN 91  
 Db 32 PVV-NFTIKVTGLAVLQWKNRPQEQGNVLEV-----QVAINMPK-EDDETERT 82  
 Oy 92 ERICQV-----GSCSTNSESKEPSILVEKIS-----PPGDPESAVTELQCIWNL--- 140  
 Db 83 ESKCVTLHKGSASVRIITLONDHSLASVNASAEIHAAPGSGPTSIYVLTCTTTEDN 142  
 Oy 140 -----SY---MKCSWLPGRNTSPDNTLYYHRSLEKIHOCENIFRE--GGYFGCSFDL 189  
 Db 143 YSRLSYOVSLHCTWLVGTADAPEDTOFLYRYGSWTE--ECQYKSKDTGLGNINACWEP 200  
 Oy 190 TKVNDSEFOHSVOIWMKNACKIKPSNIYPLTSRVKPDPPHINKLSFHNDLYVOMEN 249  
 Db 201 TILISKGDMLAVLNVNGSSKSHAIRPDQLFALHIDQINPLANTALEGTRLSIQWEX 260  
 Oy 250 PON-FISCLPEVEVANNOSQETIHANVFYQEKACENPEPERNVENTSCMPVGVLPDLIN 308  
 Db 261 PVSAPPHICFDEYVNIHNTFRG-----YLOEKLMTNFIISIDLSKY----- 305  
 Oy 309 TVIRIKTNKLCYEDDKLMSNMGSISIGK 338  
 Db 305 DVQVRAAVSSMKREAG-LMSEMSQPIYYGK 333

## RESULT 8

014431 PRELIMINARY: PRT: 410 AA.

AC 014431  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE GM-CSF RECEPTOR.  
 OS Homo sapiens (Human).  
 OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91352066.  
 RA CROSTIER K.E., WONG G.G., MATHEY-REVOT B., NATHAN D.G., STEFF C.A.;  
 RT "A functional isoform of the human granulocyte/macrophage  
 colony-stimulating factor receptor has an unusual cytoplasmic  
 domain";  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).  
 DR EMBL: M64445; AAA35908.1; .  
 KW Transmembrane.  
 SQ SEQUENCE 410 AA: 46901 MW; 30CE1609 CRC32;

Query Match 9.5%; Score 221.5; DB 4; Length 410;  
 Best local similarity 22.4%; Pred. No. 1.4e-11;  
 Matches 88; Conservative 75; Mismatches 178; Indels 51; Gaps 17;

Oy 31 TOPPTNLVSVENLCVITWMPNPEGAS-SNCSLWTFSHRGDKQKRIAPETRSIEVP 89  
 Db 29 TVAPASSLNVAFDNR-TWNLSMDCQENTFSKFL-----TDKKNRYVEERLSNNECSC 81  
 Oy 90 LNERICLVGSCSTNSESKEPSILVEKISPPEDPESAVTELQCIWNLSTYKCSWLP 149  
 Db 82 TFERICLHEGVTFFEVHNTSQRGFQKLLYPNSGEGTAQNFSCFIYNADLMCTVARG 141  
 Oy 150 RNTSPDNTLYYHRSLEKIHOCENIFRE--GGYFGCSFDL-TKVKDSEFOHSVOIWMK 207  
 Db 142 PTPRPDVOYFLYIKRSKRREIKRPIYQDSGTGVGHLDLSGLTSKNY-----FLVN 195  
 Oy 208 DNAGIKRPF--NIYPLTSRVKPDPPHINKLSFHNDLYVOMENPQNF--ISRCLF-YEV 262  
 Db 196 GTSREIGIOFDSLDTYKIKETFNPSNVTVRCNTHCLVWKKPRTYQKLSYLDFOYOL 255  
 Oy 263 EVN--NSQETIHANVFYQEKACENPEPERNVENTSCMPVGVLPDLINTVIRKTNKLC 320  
 Db 256 DVHRRNTPGTENLLINVSGLENR-----TNFSSSEPRAKSHVIRADVRIL 304  
 Oy 321 YEDDLMSNMGSISIGKRNS--TLYTMLLIVPIYAGALIVLLYLKRLKI-TIEPP 377  
 Db 305 N-----WSWSEALIEFGSDDNLSGVYIYVLLVIGTLVCG--IVLGLFKRLRIQRLEFP 358  
 Oy 378 IP-----DPGKIFKFNFGQNDTLWKKRY 402  
 Db 359 VPQIKDKLNDHNEVEDEN-GPQRHRCGMNLY 389

## RESULT 9

018880 PRELIMINARY: PRT: 296 AA.

AC 018880  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE PROLACTIN RECEPTOR SHORT FORM.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97375450.  
 RA SCHULER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;  
 RT "Prolactin receptor heterogeneity in bovine fetal and maternal  
 tissues";  
 RL Endocrinology 138:3187-3194(1997).  
 DR EMBL: AF027403; AAB83999.1; .  
 DR FEMM; PF00041; fn3; 2.  
 SQ SEQUENCE 296 AA: 33854 MW; 8B40CCD8 CRC32;

## Query Match

7.8%; Score 182; DB 6; Length 296;



Best Local Similarity 24.3%, Prec. No. 2.7e-08;  
Matches 72; Conservative 41; Mismatches 111; Indels 72; Gaps 13;

QY 108 EXPSTIVEKICISPPGDESAVTELOCIMHNSYKCSWLPGRNTPSPDNTLYYHNSL 167  
DB 29 EKPRLV--KCRSPGK-----ETFTCWEPGADGLPTNTLYYHNSL 69  
QY 168 EKHOCENIFREGOYFGSFDLTWKYKSSFEQHSVOIWKDNAGKIKPSFNIPLTSRYK 227  
DB 70 TLHHCSPD-YKRGSPNSCYF--SKKHTSIWKMYVITVANAINGMSSSDPLVHTYIYE 126  
QY 228 PDPPHKLUSF--HND--LYQWENPN-----FISRCLEYEVENNSQT---E 270  
DB 127 PEPP--ANLTLELKHEDRKPPLMIKSPPTMTDVKSGWFI---IQYEIRLKEKATDWE 181  
QY 271 THNVYVOEAKCENPEFENVENTSCFMPVGLPDTLNTVRIRVTKNKICYEDDKLMSW 330  
DB 182 THFTLKQTLKIFN-----LYPGOKYLVQIR-----CKPDHGYSWM 218  
QY 331 SOEMSGIKRKNSTLYITMLIVPVIAGAIYVLLYLKRLK-----IIFPPIPP 381  
DB 219 SPESIOIIPNDPPVADTSMIVFALISAVICIMWANAVALKGSMTCTILPPVGP 274

RESULT 10

093404 ID 093404 PRELIMINARY: PRT: 346 AA.  
AC 093404;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE PROLACTIN RECEPTOR (FRAGMENT).  
OS Oreochochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
CC Neopterygii; Teleostei; Acanthopterygii; Perciformes;  
CC Perciformes; Labroidae; Cichlidae; Tilapia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-GILL.  
RA SHIRAIISHI K., MATSUDA M., MORI T., TETSUYA H.;  
RT "Expression of prolactin and cortisol receptor gene in early-life  
stages of tilapia (Oreochochromis mossambicus)."  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF080247; AAC31825.1;  
DR PFM: PF00041; fn3; 2.  
FT NON-TER 346  
SQ SEQUENCE 346 AA; 39203 MM; 1E8A63B9 CRC32;

Query Match 7.6%, Score 177; DB 13; Length 346;  
Best Local Similarity 22.4%, Pred. No. 8.9e-08;  
Matches 64; Conservative 40; Mismatches 104; Indels 78; Gaps 11;

QY 130 TELOCIMHNSYKCSWLPGRNTPSPDNTLYYHNSL 167  
DB 33 TEICRSPKEKFTCMWPGSDGLPTLYALYKREGSDVYHECPDYHAGKN-SCFEN- 91  
QY 190 TKVKSSEFQHSVOIWKDNAGKIKPSFNIPLTSRYK 227  
DB 91 -KNDTLIWSYITVAVNALGKRTSDPYDIDVYIVKHPREKLEVITMKOGMPFLV 149  
QY 246 QWENPONTISR--CLFEYEV--NNSQTEH--NVEYVOEAKCENPEFER 289  
DB 150 SWEPHKAADTRGKWTILYELAVKLEDESEVENNAAGQKFNIFSLRSG----- 201  
QY 230 NVENTSCFMPVGLPDTLNTVRIRVTKNKICYEDDKLMSW 330  
DB 201 -----GTYLIQVR-----CKPDHGYSWM 218  
QY 349 -----LLIVPVIAGAIYVLLYLKRLK-----IIFPPIPP 381  
DB 229 AYLHREKSWIILVYVSAFILLIWLIONSHSLKHCMLPPVGP 274

RESULT 11  
QY 046561 PRELIMINARY: PRT: 581 AA.  
AC 046561;  
DT 01-JUN-1978 (TREMBlrel. 06, Created)  
DT 01-JUN-1993 (TREMBlrel. 06, Last sequence update)  
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.  
OS Ovis aries (sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
CC Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
CC Caprinae; Ovis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE: 98001468.  
RA BIGSON C., BIRNAT N., ORMANDY C., SCHULER L.A., KELLY P.A.,  
R. DJANE J.;  
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning  
and genomic analysis reveal that the two forms arise by different  
alternative splicing mechanisms in ruminants and in rodents."  
RT J. Mol. Endocrinol. 19:109-120(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA BIGSON C., DJANE J.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DE EMBL: AF041257; AAB96795.1;  
DR PFM: PF00041; fn3; 2.  
FT SIGNAL 1  
FT CHAIN 24  
SQ SEQUENCE 581 AA; 65235 MM; 6792A7C7 CRC32;

Query Match 7.5%, Score 175; DB 6; Length 581;  
Best Local Similarity 23.8%, Pred. No. 2.6e-07;  
Matches 78; Conservative 46; Mismatches 116; Indels 88; Gaps 16;

QY 108 EXPSTIVEKICISPPGDESAVTELOCIMHNSYKCSWLPGRNTPSPDNTLYYHNSL 167  
DB 29 EKPRLV--KCRSPGK-----ETFTCWEPGADGLPTNTLYYHNSL 69  
QY 168 EKHOCENIFREGOYFGSFDLTWKYKSSFEQHSVOIWKDNAGKIKPSFNIPLTSRYK 227  
DB 70 TLHHCSPD-YKRGSPNSCYF--SKKHTSIWKMYVITVANAINGMSSSDPLVHTYIYE 126  
QY 228 PDPPHKLUSF--HND--LYQWENPN-----FISRCLEYEVENNSQT---ET 271  
DB 127 PEPP--ANLTLELKHEDRKPPLMIKSPPTMTDVKSGWFI---IQYEIRLKEKATDWE 182  
QY 271 HNVYVOEAKCENPEFENVENTSCFMPVGLPDTLNTVRIRVTKNKICYEDDKLMSW 331  
DB 182 THFTLKQTLKIFN-----LYPGOKYLVQIR-----CKPDHGYSWM 218  
QY 331 SOEMSGIKRKNSTLYITMLIVPVIAGAIYVLLYLKRLK-----IIFPPIPP 381  
DB 219 SPESIOIIPNDPPVADTSMIVFALISAVICIMWANAVALKGSMTCTILPPVGP 274

RESULT 12

075462 ID 075462 PRELIMINARY: PRT: 422 AA.  
AC 075462;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.  
GR CLF-1.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA ELSON G.C.A., GABER P., LOSBERGER P., HERREN S., GREYNER D.,  
 RA MONOD L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.,  
 RT "GIF-1, a Novel Soluble Protein Shares Homology with Members of the  
 RT Cytokine Type-1 Receptor Family.",  
 RL J. Immunol. 0:0-0(1998).  
 DR EMBL: AF059293; AAC28335.1;  
 DR PRAM: PF00041; fn3; 2.  
 KW Signal.  
 FT SIGNAL 1 37 POTENTIAL.  
 FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.  
 SO SEQUENCE 422 AA; 46301 MW; 8779BC9 CRC32;

Query Match 7.3%; Score 169.5; DB 4; Length 422;  
 Best Local Similarity 22.5%; Pred. No. 5.2e-07;  
 Matches 80; Conservative 53; Mismatches 159; Indels 63; Gaps 18;  
 QY 13 LLLCAGG---GGGGGAAPETOPPTNLVSVENICTVITWNPPEGASNCISLWFSH 69  
 DB 24 LLLCIVLGPAGASAHRAVISPOPTLLIGSLATCSV---HGDPPEATIEGLWTILN- 80  
 QY 70 FGDKODKIAETRRSIEVPLNERICLOV---SGOCSTNE---SEKPSILVEKICSP 120  
 DB 80 ---GRLPELSRVLNA---STLALALANLSRQSGNLVCHANDGSLGSCLY- 131  
 QY 121 PEGPESAVTELQCIWNLSTKCSWLFGRN--TSPTNTLYLWHSLEKIHOCENIFR 178  
 DB 131 -VGPRPEKPVNISCSMKMKDLTCRMTPGAGETFLHTNYSILKRLWYGDNDNCEEHT 189  
 QY 179 EGOYEGCSFDLTAKVD--SSEQHSQVIMVKDAGIKRSPINIVPLTSVKRDP--HIK 234  
 DB 190 VGP-SCHIP---KDALFTPEIWEATNRLSASDVLTLDLVYTTDPPDVHVS 244  
 QY 235 NLSEHNDLYQWENP---QNFISRCLE---YEVEVNSQTEHNVFVQAKCENPEFE 288  
 DB 245 RVGLLEQGLSVRWSPALKDFLFOAKQIRYEDSDVMKVVDDY----- 291  
 QY 289 RNVENTSCFVPGVLPDLTNTVRIRVTKNKLCEYEDK--LMSNMSQESICKKN 341  
 DB 291 --SNQTSCLAGLKPGLVYFVQVRCNPFGL--YGSKKAGIWEWSHPYASTPRS 341

RESULT 13  
 057519  
 ID 057519 PRELIMINARY; PRT; 881 AA.  
 AC 057519;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
 DE Gp130P1.  
 GN XGP130.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
 OC Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae;  
 OC Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA CHEN J., GRACE A., CHEN K.R.,  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041845; AAC03531.1;  
 DR PRAM: PF00041; fn3; 4  
 SO SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;

Query Match 7.1%; Score 164; DB 13; Length 881;  
 Best Local Similarity 25.3%; Pred. No. 4.1e-06;  
 Matches 56; Conservative 32; Mismatches 81; Indels 58; Gaps 10;  
 QY 123 GDESAVTELOCIWNLSTKCSWLFGRNTPNTLYL--YWHRSLEKIHOCENIFREGO 181

DB 119 GLPDKPFTNLCTIYVNDNLCTWDPGRPTNLPTNTLSHRW-----A 161  
 QY 182 YFGSFDLTAKVKSSEFQHS-----VOIMVNDKAKIRSPINIVPLTSVKRDP 231  
 DB 162 HFGANY--CGGANNSTHSPGFQFYDTTFQVEANTELQSELTLPVNVKPNP 219  
 QY 232 H---IKNLSEHNDLYQWENPQNFISRCLEFEVEVNSQTEHNVFY--VOEAKCENP 285  
 DB 220 QLSLISLSLEPN-ALKIEKNP-----ITNPNKINRYRVPVTKQEMW 265  
 QY 286 EFERVENTSCFVPGVLPDLTNTVRIRVTKNKLCEYED--KIMSWSQ 332  
 DB 266 PEEDTASHPSFTLQDLPNTVVEVSIR-----CIHKDGHGFWSDMSE 308  
 RESULT 14  
 016564  
 ID 016564 PRELIMINARY; PRT; 333 AA.  
 AC 016564;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)  
 DE GM-CSF RECEPTOR PRECURSOR.  
 OC Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91376112.  
 RA RAINES M.A., LIU L., QUAN S.G., JOE V., DIPERSIO J.F., GOLDE D.W.,  
 RT "Identification and molecular cloning of a soluble human  
 RT granulocyte-macrophage colony-stimulating factor receptor.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PLACENTA;  
 RX MEDLINE; 91088339.  
 RA ASHWORTH A., KRAFT A.,  
 RT "Cloning of a potentially soluble receptor for human GM-CSF",  
 RL Nucleic Acids Res. 18:7178-7178(1990).  
 DR EMBL: W73832; AAA35909.1;  
 DR EMBL: X54935; CAA38697.1;  
 KW Signal; Alternative splicing.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 333 GM-CSF RECEPTOR.  
 SO SEQUENCE 333 AA; 38438 MW; 48178079 CRC32;

Query Match 7.0%; Score 162.5; DB 4; Length 333;  
 Best Local Similarity 20.5%; Pred. No. 1.6e-06;  
 Matches 65; Conservative 61; Mismatches 152; Indels 39; Gaps 12;  
 QY 31 TQPTNLVSVENICTVITWNPPEGAS--SNCSLWFSHFQKODKIAETRRSIEVP 89  
 DB 29 TVAPASLLNRFDSR--TNLSMDCQENTTFSCFL-----TDKKNVVPRSLNNECSC 81  
 QY 90 LNERICQVQSQCSTNSEKPSILVEKICSPPEGDESAVTELOCIWNLSTKCSWLP 149  
 DB 82 TFEICLHEGVTEVHVNTSQRGFQKLLPNSGREGTAQNFSCFLYNDLNCWTWARG 141  
 QY 150 RNTSPDNTLYLWHSLEKIHOCENIFRE--GOYFGSPD-LTKVDSSEQHSQVQIMVK 207  
 DB 142 PTAPRDVQFLYIRNSKRREIRCPYIYQDSGTHGVGHDLNLSGLNSRN-----FLVN 155  
 QY 208 DNAGKIRPSP--NIVPLTSVKRDPDPHIKNLSFHNDLYQWENPQNF--ISRCLE- YEV 262  
 DB 196 GTSREICIQFSDSLDKTKIERPNPNSVNTVRCNTHTCLVRMKOPRYQKLSYLDFOYOL 255  
 QY 263 EVN--NSQTEHNVFYQAEKCNPEFERVENTSCFVPGVLPDLTNTVRIRVTKNKL 320  
 DB 256 DVHRKNVQPTGENTLLNVSGDLENR-----YNPSSSEPRAKHSVIRAAADVRL 304

OY 321 YEDDKLMSNMSQMSIG 337  
DB 305 N-----WSSWSEAIERFG 316

RESULT 15

064146 PRELIMINARY; PRT; 896 AA.  
AC 064146;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
DT 01-NOV-1998 (TREMblrel. 08, last annotation update)  
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).  
GN RIL-3R<BETA>.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95370942.  
RA APPEL R., BUTTINI M., SAUTER A., GEBICKE-HARTER P.J.;  
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured  
microglia and its mRNA expression in vivo."  
RL J. Neurosci. 15:5809-5809 (1995).  
[2]  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WISTAR; TISSUE-BRAIN;  
RA GEBICKE-HARTER P.J.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; 579263; AAB35068.1; .  
DR EMBL; AJ000555; CAA04186.1; .  
DR PFAAM; PF00041; fn3; 2.  
KW Signal.  
FT NON\_TER 1 1  
FT NON\_TER 896 896  
SQ SEQUENCE 896 AA; 99504 MW; 8E7ED2CD CRC32;

Query Match 6.6%; Score 154.5; DB 11; Length 896;  
Best Local Similarity 24.2%; Pred No. 2.8e-05;  
Matches 86; Conservative 53; Mismatches 140; Indels 77; Gaps 20;

OY 51 TNNPREGASS--NCSLMYSHFGDKQDKIAPTRRSIEVPLNERICLOYSQSCSTNESE 108  
DB 184 SW---EDASSLHCNLMV-----TLEPKLFLP---NSTIV-ARYRAQLAPGSSLSGRPSG 231  
OY 109 -KPSILVEKCI SPPEGDPEAVTELQCIWHNLSYMKCSMLPGKNTSPDTNYTLYYHRSLS 167  
DB 232 WSPFVHMD--SPTF--DKARPONLQCFEDGIQSLNCSWMTKVTDSVSFGLFYSSSPK 286  
OY 168 EKHOCENIFREGO-----YFGCSFDLTKVKSDFEHSQIWMKNDAGIKRPSFNVPL 222  
DB 287 AGEKKCSPPYKELQASRYTRYHCSLANS--DPAHSQIYTSV-RLKQGFISFN---- 340  
OY 223 TSHKDPDPPIHKNLSFHNLDLYQWENPQNFISRCLEFEVENNSQTEHNVFYVEAK- 282  
DB 340 --HIQNNPPTL-NLTKNRPSYSLHWETQK-----MSYPFIQHAFQVQYKKK 382  
OY 282 ---CENPEPERNVENTSCFVPGVLPDNLTVIRYKTKNKLCTEDDKLMSNMSQMSIGK 338  
DB 383 LDWEDSKTE-NLNHAHSMDLPLEPSTSYCAHRYKT--IPEYKGLWSEMSNECTW-- 437  
OY 339 KRNSTLYITMLLVPIYVAGAIIVLLYL-----KRLKIIIFPIPDGK 383  
DB 437 ---TIDWVNPFTLWIVILVFLILTFLLALRFQCIYGCCKLYRRWK---EKIPNPSK 485

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**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4009	100.0	4009	5	A63237	A63237 Sequence 3
2	3999	99.8	3999	9	HS1IL13RA1	Y09328 H.sapiens m
3	3995	99.7	4039	9	HS1IL13RA	X10659 H.sapiens I
4	1697	42.3	1708	41	HSU081379	U81379 Homo sapien
5	1467.2	36.6	1572	11	HSU063858	U62878 Homo inter
6	976.2	24.4	1660	12	SS09633	SS09633 NR4-IL-13
7	862	11.5	1099	41	AF074430	U81380 Homo inter
8	817.5	30.4	1048	3	AF074432	AF074402 Bos tauru
9	281.8	7.0	458	13	G29664	G296644 Human STR
10	260	6.5	134578	33	AC004824	AC004824 Homo sap
11	253.6	6.3	141857	42	AC010532	AC010532 Homo sap
12	253.4	6.3	176357	33	CMS01DR	AL118536 Homo sap
13	252.8	6.3	132647	33	HS785G19	AL035458 Homo sap
14	251.4	6.3	152878	33	HSJ0746H2	AL109953 Homo sap
15	251.4	6.3	148091	33	HSJ0746H1	AL117352 Homo sap
16	250	6.2	114939	9	AP000050	AP000050 Homo sap
17	250	6.2	151516	9	AP000117	AP000117 Homo sap
18	250	6.2	100000	9	AP000193	AP000193 Homo sap
19	250	6.2	78539	9	AP000313	AP000313 Homo sap
20	250	6.2	96625	11	HSAC000118	AC000118 Human BAC
21	249.8	6.2	146523	41	AC004953	AC004953 Homo sap
22	249.4	6.2	196532	11	AC002365	AC002365 Homo sap
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24	249.2	6.2	103083	33	AP000424	AP000424 Homo sap
25	248.5	6.2	171040	42	AC008623	AC008623 Homo sap
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33	246.8	6.2	123339	43	AF179296	AF179296 Homo sap
34	246.6	6.2	129577	11	AC004659	AC004659 Homo sap
35	246.4	6.1	119330	10	HS12803	AC004659 Homo sap
36	246.4	6.1	90389	11	AC004008	AC004008 Human PAC
37	246.4	6.1	276261	33	HSAC000406	AC004006 Homo sap
38	246.2	6.1	233192	43	AC009600	AC009600 Homo sap
39	246.2	6.1	163027	11	AC002549	AC002549 Homo sap
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43	245.8	6.1	42030	41	AC007565	AC007565 Homo sap
44	245.6	6.1	166181	10	HS376L6	Z83844 Human DNA
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NTD	03717098				
VECTION	A63257.1	GI:3717098			
KEYWORDS	unclassified.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1. (bases 1 to 4009)				
ADVISORS	Caputi, D., Ferrara, E., Laurent, P., Vita and Natalio.				
TITLE	IL-13 RECEPTOR POLYPEPTIDE				
JOURNAL	Patent: WO 9720926-A 3 12-JUN-1997;				
	S4NORI SA (FR)				
COMMENT	Other publication AU 7576096 1997067				
	Other publication FR 2742156 19970613.				
DESCRIPTORS	Location/Qualifiers				

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/db\_xref="taxon:32644"  
/cell\_line="LJLAIRE: CARI-1"  
BASE COUNT 1137 a 826 c 882 g 1164 t  
ORIGIN

Query Match 100.0%; Score 4009; DB 5; Length 4009;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4009; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 tcacccggcgccggcgctccggcgagagagcgtgcataagtgagcgcgcggtctcgagg 60  
1 TCACCCGGCGCGCGCTCCGGCGAGAGAGCGTCATGAGTGGCGCGCGCGCTCTCGCGG 60  
61 ctgtggcgctgtctgtctgtcgccgagcgagcgagcgagcgagcgagcgagcgag 120  
61 CTGTGGCGCTGTCTGTCTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
121 gaaactgagccactgtgacaaatttgatgtctgtgtgaaaaacctctgcacagtaata 180  
121 GAAACTGAGCCACTGTGACAAATTGATGTCTGTGAAAAACCTCTGCACAGTAATA 180  
181 tggacatgagatccaccggaggagccagctcaattgtgtctatgtatgtatgtatcat 240  
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241 ttggcgagcaacaagaataagaataagctcggaaactgcgtcctcaataagaatcccc 300  
241 TTGGCGAGCAACAAGAATAAGAATAAGCTCGGAAACTGCTCTCAATAAGAACTACC 300  
301 ctgaagcgagagattgtgtcgcagagtgagggtccagtgtagcccaatgagagtgagag 360  
301 CTGAAGCGAGAGATTGTGTGCGAGTGAGGTTCCAGTGTAGCAACCAATAGAGTGAAG 360  
361 cctagcatcttggtgtgaaaaatgcatctcaccgccagagagtgatctcgtagctgtgtg 420  
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721 cctccagatataaaaactctctctcccaaatgagactatgtgtaaatgagagagat 780  
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781 CCACAGAAATTATATAGAGATGCTATTTATGAAAGTAAAGTCAATACAGCAACT 840  
841 gagcacataatgtttctcactgtccaaagaggtataatgtgtaaatccagaattgagaga 900  
841 GAGCACATAATGTTTCTCAGTGTCCAAAGAGGCTAAATGTGAAATCCAGAAATTGAGAGA 900  
901 aatgtgagataataatctgtttcaatgtgtcccggtgttctctcgtactatgtaacaca 960

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Qy 1081 ctcattgtccagtcactgtcgacagtgacatcaatgactccttcttactataaagg 1140  
Db 1081 CTCATTGTTCCAGTCACTGTCAGAGTGCATATCATATGATCTCTTACTTAAAGAG 1140  
Qy 1141 ctcaagattatataatctccctcaattccctgataccctggaagattttaaagaatgtt 1200  
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Db 1801 GCTATTAAACCTTTTAAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
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 Db 2761 CAGAGATTAATAGCAGATCAGAGTAAAGTGAATGAGTGAATGAGTGAATGAGTGAAT 2820  
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 Db 2881 ATGATTAATTAATAGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 2940  
 Qy 2941 ATGCTTTGGGGGAGATTAATGAGTTCATCTCCATCCATCCATCCATCCATCCATCC 3000  
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 Db 3001 ATATCCCTCTACTCTACTCTACTCTACTCTACTCTACTCTACTCTACTCTACTCTACT 3060  
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Qy 3121 TTAATTCAGAGTGTCTCAACATTTCAACATTTCAACATTTCAACATTTCAACATTT 3180  
 Db 3121 TTAATTCAGAGTGTCTCAACATTTCAACATTTCAACATTTCAACATTTCAACATTT 3180  
 Qy 3181 TCTGTCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240  
 Db 3181 TCTGTCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240  
 Qy 3241 GGAAGCT 3300  
 Db 3241 GGAAGCT 3300  
 Qy 3301 GGTTCATGACAAATGACAGATGTAATTTCTCTGAGTCAAGTTAGAGCTGGAGACAG 3360  
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 Db 3781 GCTATGATGATTTTCTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCA 3840  
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 Db 3841 ATTCTTTGCTCAATTTTCTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCT 3900  
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 Db 3901 TGTAACTTTTGTGAGTCTTCAACAGGAGTGTCTTGTGTTAATCTTTTATAGGAA 3960  
 Qy 3961 GCTTGTGATTAATTAATTTGCTTTTGTGATGTCACCCCAAAAAA 4009  
 Db 3961 GCTTGTGATTAATTAATTTGCTTTTGTGATGTCACCCCAAAAAA 4009

RESULT 2  
 HSL13R1 3999 bp mRNA PRI 26-FEB-1997  
 LOCUS H.sapiens mRNA for h13 receptor alpha-1 chain.  
 DEFINITION ACCESSION Y09328  
 VERSION Y09328.1 GI:1885307  
 KEYWORDS alpha 1 chain; HSL13R1 gene; Interleukin-13 receptor.  
 SOURCE human  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;





Db	1501	TTGGAGAAGACTCTGGAGCTATTCTCATTTGAATTATAAAGCAGAGGCTCAAACTAG	1560
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Db	1561	GGGACAAAGCAAAAAGAGATAGTGTGAGATTATCTTATCTTCAAGAGTGTGCAACT	1620
Qy	1621	tccgagggagatctatctgtcttgtgttccttgtgttcaacgtgaacattttctgt	1680
Db	1621	TCCTGAGGAGATCTACTTGTCTTGTGTCTTGTGTCTCAACTGAACTAATTTATTTGT	1680
Qy	1661	agggaaactccatttgggtgtgcaaatgtcaatgttcaactgtgtccaaagacatag	1740
Db	1661	AGGGGAAGCTCTTTGGGTGCAAACTGCTAATGTCAAACTTGATGTACAAAGAACATGTAG	1740
Qy	1741	aaaaaacaatgagataaatttgtatgtatgtgttgggttcctattgaaactgtgttg	1800
Db	1741	AAAACAAAATGGATAAATATGTATGTATGTATGTTGGATTCCTATTTGAACCACTGTTTGTG	1800
Qy	1801	gctaataaacctctttaaacaagctgtggtctgtgtccgtgtgtctcaagccctgtaaaccag	1860
Db	1801	GCTATTAAACTCTTTTAAACAGCTGGGGTGGGTCCGGTGGCTCAAGCCTGTAAATCCAG	1860
Qy	1861	caatttggagatccgagcggtgcgtacatcctgaggtcaggaagttccagaccagcttgc	1920
Db	1861	CAATTTGGGAGTCCGAGCGCGGGGATCTCGAGTCCGAGGTCCAGACCGAGCTTAC	1920
Qy	1921	caaaatgtgaaaccttcctctctactaaacatacaaaaataaactcgtggtgtgtgtgcg	1980
Db	1921	CAAAATGTGAACCTCTCTCTTACTTAATAACTACAAAATTACTGTGGTGTGTGTGGCCG	1980
Qy	1981	tgcctgtaatcccaagctactcctgtggaagctgtgagcgatgaattgtttgaacctgtggaagt	2040
Db	1981	TGCGTGTAAATCCCAAGCTACTCTCGGGAAGCTGAGCAGTGAATGTTTGAACCTGGGAGGT	2040
Qy	2041	ggaaagtgtcagttgagcgagaaatacaaccactgtgaactcgtcgtgtgtgtgacagaaagaaac	2100
Db	2041	GGAGGTTGCACTGTGACGAGATATCACCACTGACACTGTAGCTGGGTGACAGAGCAAAAC	2100
Qy	2101	tccttcataaaaaaacaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac	2160
Db	2101	TCCTGTAAAAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACCTGTATATCTGGAGT	2160
Qy	2161	catcaatccctctgcagcagcaatcttcctctgtcttgaagagccccaagaatcagtgctgccc	2220
Db	2161	CATATTTCCTTGGACAGCAATTTCTCTGTCTTGTGAACCCCAAGAAACATGTTGTGCC	2220
Qy	2221	atgatagaactataagaanaaacagcagcgagctctcttgcagaagaccttcaagcaact	2280
Db	2221	ATGATGACAACTACAGAAAACAGAGGACGCTCTTTGCCAAGACCTTTCAAAACCAATT	2280
Qy	2281	ttaagctgtttagggcaggtgaggtagaatgacatccttggatataagatttaacaacatg	2340
Db	2281	TTAGGCTGTTAGGGCGAGTGGAGGTGAATGACCTCTTGGATTAGAGTTCAACCATAG	2340
Qy	2341	aagcgtctaacaatgatatcttctcaactcctgtactcaatgagatattacgttctt	2400
Db	2341	AAGCTCTAACAAATGATATTTCTTCACTCTGTGACTCAAGTAGCACTTACGTCTCTTT	2400
Qy	2401	ggtttgtctaggccccccgggtgtgagacacagaccccttcaaggggtttaaagctat	2460
Db	2401	GGTTGTGCTAGGGCCCCGGGTGTGAAGCAGACCCCTTCAGGGGTTTACAGCTAT	2460
Qy	2461	tgaagacctccagttctctgtgcacatttttttttaactccacacagtcattttcagaect	2520
Db	2461	TGAAGCTCTCAAGTCTTGTGGCACTTTTTTTTTTAACTCCACCAAGTCAATTTTTCAGACT	2520
Qy	2521	tttaaccctccaattccaacaacagattccccccttgtgacatctccctcctccctct	2580
Db	2521	TTTAACCTCCCAATTCACAACAGATTTCCTTTGCAATCTCCCTCTCTCCCTCTCTT	2580
Qy	2581	gtagacctttgaacttcaattgaaattagatgataaactcgtctraggaacctgtgagag	2640

[illegible]

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BASE COUNT      . 1135 a   . 839 c   . 896 g   . 1169 t
ORIGIN

Query Match          99.7% Score 3995; DB 9; Length 4039;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3995; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB       12 CAGCCCGGCGGGCTCTCCGAGGAGAGCGTGCATGAGAGTGCGCGCGCCTCTCCGGGC 71
QX       62 tgttgagcgtctgtctcttcgcccgcgcggcgggcgggcgggcgggcgccgctacgg 121
DB       72 TGTGGCGCTGCTGCTGTGCGCTGCGCGCGCGGGGGGGGGGGGGCGCGCGCGCTACGG 131
QY       122 aaaccagccacctgtgcacaattttagtgcctcgtttgaaacctctgcacagtaaat 181
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QY       182 ggacattgatccaccgccgagggagccagctcaatttgtatctatgttatagtcatt 241
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QY       242 ttggcgacaaacaagaataagaanaatagctccggaactcgtcttcaatagaatcccc 301
DB       252 TTGGCGAACAAACAAGATAGAATAATACCTCCGMAACTCGTCTCAATGAAGTACCCC 311
QY       302 tgaatgaaggaatttgcctcgaagtggggtccagtgtagcaccaatlgagtgaaagc 361
DB       312 TGATGAGAGGATTTGTCTGACAGTGGGCTCCAGTGTGACCAATGAGAGTGAAGAC 371
QY       362 ctgacatttggfittgaaaaatgcatctcaaccgccaaaagtgtatcccttgatgctgtga 421
DB       372 CTAGCAATTTGGTTGAAAAATGCATCTCACCCCCAGAAAGTATCTGATGTGCTGTGA 431
QY       422 ctgagcttcaatgcatlttgycacaaccttgagtaataatgaagtgtcttggctcccttga 481
DB       432 CTGAGCTTCAATGCAATTTGGGCACACCTGAGTAAATAGTAAGTGTTCTTGCGCTCGAA 491
QY       482 ggaataccaggtccgaacatactaactcttactattgtgcacagaagccttgaaaaaa 541
DB       492 GGAATACCAAGTCCGACACTACTACTCTCTCTACTATTGTGCACAGAAGCCTGGAAAAA 551
QY       542 ttcatcaatgtgaaaaacactcttttagagaagccataacttggttgtctcctttgaticga 601
DB       552 TTCATCATGTGAAAACAATCTTTAGAGAAGGCCAATCTTTGGTGTTCCTTTGATCGA 611
QY       602 ccagaatgaagatltccaagtttgaacaacagltgccaatatgtttaagatgat 661
DB       612 CCAGAGTGAAGGATTCAGGTTTGAACMACACAGTGTCCAATATATGTGTAAGGATPATG 671
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DB       672 CAGGAAAAAATTAACCACTCTTCAATATAGTGCCTTAATCTTCCGCTGGAACCTGATC 731
QY       732 ctccacatataaaacctccttcacaatgtatgacatatatgtgtggaatc 781
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QY       782 cacagaatttlatcacagatgcctatltttagaagttagaagtaacaacagccaaacty 841
DB       792 CACAGAAATTTATTTAGCANATGCCATATTTTAAAGAGTGAAMATCAATTAACGCCAAACG 851
QY       842 agaacatatatgttttctaagtcacaagaggtcaaatgtggaatccagaatttggagaa 901
DB       852 AACACATATATGTTTTACGTCACAAGAGGCTAATGTGAATATCCAGAAATTTGAGAAA 911
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DB       912 ATGGGAAATATACATCTTGTTTCAATGCTGCTGATGTTCTTCCGATACATTGAAACAG 971
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 Db 2652 AGAGATTAATTAAGCATCTCAGGTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2711  
 Qy 2702 gcatatttgaactcctcagtgaggttttcaagcatgataattgtcattcttaac 2761  
 Db 2712 GCATTTTGTATACCTCATGATGAGGTTTTCAGATGATTTGTGATTTTTCATAC 2771  
 Qy 2762 agagatg+ggtgtatcttcaagtagaactgtgattcgtctgagaaacaaagatgt 2821  
 Db 2772 AGCATGAGAGGTGATCTTCACTGAGAACATGCTGATTCGTTGAGAAAAAAGATAGT 2831  
 Qy 2822 tgaacatcttctccttctttaaagaatgagtgagaggttccctcttctcgcataaa 2881  
 Db 2832 TGAACCTAATTCCTCTTTTAAAGATGGGTCCAGATTCCTCTTCTGCGCATAAA 2891  
 Qy 2882 tgaatcaataaagccttctgtcttcaatgtagcagcagcagcagcagcagcagcagc 2941  
 Db 2892 TGATTAATTAATNCTTTGTGCTTACATTTGTAAGCAGACCAAGAGCTGCTTA 2951  
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 Qy 3002 tat+ccctcactcttactccccaatttaagaagaatagaggaatgagaggaattc 3061  
 Db 3012 TATCCCTACTACTCTTCTCCCTAAATTTAAAGATGAGGAAATGAGGAGATTTT 3071  
 Qy 3062 cccgcccacattctctcctcaacacagacacacacacacacacacacacacacacacacac 3121  
 Db 3072 CCGCACCCCATTTCTCTCTCAGACACAGACATCAATTTACTGTAAGTGAAGTGAAGTGA 3131  
 Qy 3122 catt+caagttgttcaacatctcaacacacacacacacacacacacacacacacacacac 3181  
 Db 3132 TATTTCCAGTGTTCAAACATTTTCAATCATATTATATACATGATCTATTTCATTT 3191



OY	482	ggaatcacagcccgacacactatactctcactattggcaagaaagccctggaaaaa	541
Db	489	ggaatpccagcccgacacactatactctcactattggcagaaagccctggaaaaa	548
OY	542	ttcataatgfgtaaaaactctcttagaagaagccaactctgtgtctctctgtccta	601
Db	549	ttcatatcatgtgaaacatactcttttagaagaagccaactctgtgtctctgtatcga	608
OY	602	ccaaatgtaagatctccagttcttgacaacacagctgtccaataatggtcaagataatg	661
Db	609	ccaaatgtaagatctccagttcttgacaacacagctgtccaataatggtcaagataatg	668
OY	662	caggaaaaatataaacacactctctcaatatgtgctttaactctccgttggaaactgtac	721
Db	669	caggaaaaatataaacacactctctcaatatgtgctttaactctccgttggaaactgtac	728
OY	722	ctccacatataaaaaactctctctccacacatgtagactatatagtgtcgaatggaaac	781
Db	729	ctccacatataaaaaactctctctccacacatgtagactatatagtgtcgaatggaaac	788
OY	782	cacgaatttatatgaagatgtccttttatgaatgaagaatcaataacgccaactg	841
Db	789	cacgaatttatatgaagatgtccttttatgaatgaagaatcaataacgccaactg	848
OY	842	agacacataatgtttctctcaagcccaagagctaaatgtagaatccgaatttggagaa	901
Db	849	agacacataatgtttctctcaagcccaagagctaaatgtagaatccgaatttggagaa	908
OY	902	atctggggaatacatctgttttcaatggtccctgtgttcttccgtatactttgaacaa	961
Db	909	atctggggaatacatctgttttcaatggtccctgtgttcttccgtatactttgaacaa	968
OY	962	tcaaatataagtgtaaaaaacaataagttatgctataggaatgacaacactgtgaata	1021
Db	969	tcaaatataagtgtaaaaaacaataagttatgctataggaatgacaacactgtgaata	1028
OY	1022	ggagccaagaatgtagtataggttaagaagcgcaattccacactctacataaccatgttac	1081
Db	1029	ggagccaagaatgtagtataggttaagaagcgcaattccacactctacataaccatgttac	1088
OY	1082	tcattgttcacagatcatgtcgaggtgtgcaatcctagtaactctgtcttaccctaaaaagc	1141
Db	1089	tcattgttcacagatcatgtcgaggtgtgcaatcctagtaactctgtcttaccctaaaaagc	1148
OY	1142	tcaagatataataatctccctccaactctctgatactctgtgcaagaatttttaagaagaatgttg	1201
Db	1149	tcaagatataataatctccctccaactctctgatactctgtgcaagaatttttaagaagaatgttg	1208
OY	1202	gagagccgaatagatgataactctgcacctcggaagaagtaagaacatctatgtgaagcaacca	1261
Db	1209	gagagccgaatagatgataactctgcacctcggaagaagtaagaacatctatgtgaagcaacca	1268
OY	1262	aggaaggaaacccgactctgtatgtctgtatagaaaaaactgtgaagaagccctcagtgatga	1321
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OY	1322	gataattatatttaaccttcaactgtgacctgtgaagaatcttcccatctccatgtgtc	1381
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Db	1449	taagaagccacaggtcttattgtgtgagtcgcgcacgcgaaaaactaaataatlyggcgctt	1508
OY	1502	tggagaagaagtgtagatcaattctcttgaattataaaagccaagcaggtttaactgtg	1561
Db	1509	tggagaagaagtgtagatcaattctcttgaattataaaagccaagcaggtttaactgtg	1568

CY	1682	cctgaggaacataccttgccttggttcctttgtgtccacaatgaacaatttatgtta	1681
L1	1563	ggacaaaccgcaaatgatcatgtagcgaggactttaatttatcaagaacttgacaactt	1628
P3	1629	cctgaggaacataccttgccttggttcctttgtgtccacaatgaacaatttatgtta	1681
OY	1682	ggggaacatcatttggg	1698
DB	1689	ggggaacatcatttggg	1705
RESULT	5		
LOCUS	HS062858	1572 bp	mRNA PRI 30-NOV-1996
DEFINITION	Human interleukin-13 receptor mRNA, complete cds.		
ACCESSION	U62858		
NID	gi:655375		
VERSION	U62858.1	GI:1695875	
KEYWORDS			
SOURCE	human:		
ORGANISM	Homo sapiens:		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Euthalia, P.; Primate, C.; Catarrhini; Homnidae; Homo.		
TITLE	Anan, M.J., Tayebi, N., Obidi, N.I., Puril, R.K., Modi, W.S. and Leonard, W.J.		
JOURNAL	CDNA cloning and characterization of the human interleukin-13		
REFERENCE	receptor alpha chain		
AUTHORS	. Biol. Chem. (1996) In press		
TITLE	2 (bases 1 to 1572)		
JOURNAL	Amann, M.J., Tayebi, N., Modi, W.S. and Leonard, W.J.		
REFERENCE	Submitted (02-JUL-1996) Lab. of Molecular Immunology, NHLBI, NIH,		
AUTHORS	9000 Rockville Pike, Bethesda, MD 20892-1674, USA		
TITLE	Location/Qualifiers		
FEATURES	1..1572		
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CDIS	/db_xref="taxon:9606"		
	/chromosome="X"		
	85..1368		
	/function="cytokine receptor"		
	/note="IL-13 receptor; IL-13R or IL-13alpha; this protein		
	together with the 140 kDa IL-4 binding protein, IL-4R or		
	IL-Ralpha, can form a functional receptor for IL-13;		
	the IL-13 plus IL-4R is also one of the functional forms of		
	the IL-4 receptor, the other is IL-4R plus the common		
	cytokine receptor gamma chain"		
	/codon_start=1		
	/product="interleukin-13 receptor"		
	/protein_id="AA837127.1"		
	/db_xref="pid:gi655376"		
	/db_xref="GI:1695876"		
	/translation="MEMPARICSMALLLAGGGGGAAPETTOPPTNLSSVEN		
	LCATITWNPPEGASMSCLWFSEFGDKODKKAIPTRRSIEVPLMERICLOYSOC		
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	YYMRSLREKHOCENIFREGFCSPDLTKVDSPFOSVOLMTVDNGKIKRPFNF		
	IIVTTSRKDDPPRIKTLSTRNDLLTYOMENPOAFIRCLFEYEVAANSOTETHNVTT		
	VOEKGKNPEPERNEVENTSCMWPGVLPTDLLTVLRIVAKTNKLCEEDKLTMSNSQEM		
	SIGKRNSTLYTMLIVPVADAIADLVLLYLRLKLIIFPIIPDPCKTFEKMFGEQD		
	NNDDLHKKKDYIKQRTKEEDSVAILLENLKASQ"		
BASE COUNT	477 a	332 c	358 g 405 t
ORIGIN			
Query Match	36.6%	Score 1467.2;	DB 11; Length 1572;
Best Local Similarity	99.1%;	Pred. No. 0;	
Matches 1475; Conservative	0;	Mismatches 13;	Indels 0; Gaps 0;

[illegible]

QY	1143	caagttctttatctccctcccaatctccgtctctgcgaagatttttaagaatgttttg	1202
Db	1194	CAAGATTTTATTTATTCCTCCCAATCTCTGATCCTGCGAAGATTTTAAAGAAATTTTGG	1253
QY	1203	aaccagaatgatgatctctgcactcgtgaagaagtacgacatcatalbgayagcaaccaa	1262
Db	1254	AAACCAAGATATGATGATCTCTGCACTGTGAAGAAAGTACGACATCTTTGAGAAACAAACAA	1313
QY	1263	gagaggaaacccgacccctgtagtgcgtatagaaaacccgtgaagaagctctcagtagtagag	1322
Db	1314	GGAGGAAACCGACACTGTAGTGCATAGAAAACCTGGAAGAAAGCCTCTCACTGATGAG	1373
QY	1323	ataattatttttacccttcactctgaccttgagaagattcttcaccattccattgltta	1382
Db	1374	ATAATTTTTATTTTACCTTCCTGACTGTGACCTTGAGAAAGATTTTCCATTCTCCATTTGTTA	1433
QY	1383	tcctgggaacttatthaatgtggaacctgaaactactgcaccatttaaaaaagcgaccat	1442
Db	1434	TCTGGGAACCTTATAGATGGAACCTGAACCTACTGCACATTTAACAAACGACGCTCAT	1493
QY	1443	aagggcacagctcttatatgtatgtagtcgagccacgcgaaaaactaaat	1490
Db	1494	AAGGACACAGGCTTTATTTTATGTCGCTTACCAAGAACCAAGAAAGT	1541

RESULT	6
LOCUS	S80963
DEFINITION	ROD 27-MAR-1997
ACCESSION	S80963
NID	580963
VERSION	619111503
KEYWORDS	S80963.1 GI:1911503
SOURCE	Mus sp. embryonal stem cell.
ORGANISM	Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus. 1 (baes 1 to 1680) Hilton,D.O., Zhang,J.G., Metcalf,D., Alexander,W.S., Nicola,N.A. and Willson,T.A. Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor Proc. Natl. Acad. Sci. U.S.A. 93 (1), 497-501 (1996)
REFERENCE	Genbank staff at the National Library of Medicine created this entry [NCBI gidsbg 175604] from the original journal article. This sequence comes from Fig. 1.
AUTHORS	Location/Qualifiers 1..1680 /organism="Mus sp." /db_xref="taxon:10095" 61..1335 /gene="ILR4" /note="IL-13 receptor alpha chain, IL-13 R alpha" 61..1335 /gene="NR4" /note="NR4" /note-"This sequence comes from Fig. 1; IL-13 R alpha" /codon_start=1 /product="IL-13 receptor alpha chain" /protein_id="AAB50695.1" /db_xref="PDB:g19111504" /db_xref="GI:19111504"
GENE	/translation="MARPALGLGELTLVLTMTATVGQVAATEVPPTNLSVENIIC TIIMTSPPEGASPNCTLRYSFSDQQOQCLAPHERKEPLDPRKCOLWSGSQA NSEEKSPYLAKCISPEEGPSAEATLCKIWHNHSMYSCMSWTPGNSTPDTHILTY WYSLEKROCENTIVREGOHINCSPFLTVPEPSFEONAVIQWDAGXIRSKCSVS LTSYVDPDPPIHLIKLKGALLVOKNQNRSRCITVEYNVTGDNRNIILEVSE DKONSSEDNMEGISTFQLPGVLADAVYTRVRINKLCEDNKNTDNMDSGAOSIG KRNSTSYFTMLLTIPVFVAVANVILLFLFKRLKTIIFPPIDPGKIFEMSGDND TLMKKYDIYERKSQKETSDVSLIEUKKAAD"
CDS	364 c 373 t 432 + 364 c 373 t 432 +
FEATURES	
SOURCE	
SEQUENCE	
BASE COUNT	511 a





/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
41.880  
/note="IL-13"  
/codon\_start=1  
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/db\_xref="GI:5174768"  
/translation="MEMBRANELCGLMALILCAGGGGGGAGAPETPTPTNLSYVEN  
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STNESKPSILVEKICISPEGPDESAVTELOCIWHLSTKSCMLPGRTSPDNTYL  
YWMRLERHOCENIFRSGQYFGESEFDLTKVDSSEFQHSVOIMKDNAGKIKPSEF  
IVPLTSRVKPDPPHINKLSFHNDLYVOMENPNFISRLIEVEVNNQSOTETHNVEY  
VRF"

BASE COUNT 311 a 231 c 254 g 303 t  
ORIGIN

Query Match 21.5%; Score 862; DB 41; Length 1099;  
Best Local Similarity 100.0%; Pred. No. 8.6e-203;  
Matches 862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 caacccggcgagcgtccgagcgagagagcgtgcatgagctgcccggcgagcgtcgcggc 61  
DB 9 CACCCGCGCGGCTCCGAGCGCAGAGGCTGATGAGTGGCGCGCGCTCTCGCGGC 68  
QY 62 tctggcgagcgtcgtcgtcgtcgcggcgagcgagcgagcgagcgagcgagcgagcg 121  
DB 69 Tctggcgagcgtcgtcgtcgtcgcggcgagcgagcgagcgagcgagcgagcgagcg 128  
QY 122 aaactaagcagcgtgacaaattgagtgctcgttgtaaaacctgtcacagtaatat 181  
DB 129 AAACAGCCACCTGTGACAAATTTGAGTGTCTGTGTAACACCTGTGACAGTATAT 188  
QY 182 ggcagtgaaatcaccgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 241  
DB 189 GGCATGAGGATCCACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 248  
QY 242 ttggcgacaaacaagaataagaataagctccggaactcgtctcaatagaatcccc 301  
DB 249 TTGGCGACAAACAAGATAAGAAATAGCTCCGAAACTGCTCTTAATGAGAGTACCCC 308  
QY 302 tgaatgagagagatttctcgcgaagtgggtcccaagtgtgacacaaatgagagtgagaagc 361  
DB 309 TGAATGAGAGGATTTCTGCAAGTGGGGTCCAGTGTGACACCAATGAGAGTGAAGAGC 368  
QY 362 cttagcatttgggttgaataatgcatctacccccagagaagtgaatcgtcgtgta 421  
DB 369 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGAGGTGATCCTGAGTGTGTTGA 428  
QY 422 ctgagctcaatgcatcttggcacaacctgagctacatgaagtgtctctgctccctgga 481  
DB 429 CTGAGCTTCAATGCAATTTGGCAACAACCTGAGGTACATGAAGTGTCTTGGCTCCGGA 488  
QY 482 ggaataccagctcccgacactaactactctactattggcagagaagccttggaaaaa 541  
DB 489 GGAATTCAGCTCCCGACACTAATCTACTACTATTTGGCAGACAGAACCTGGAAAAA 548  
QY 542 ttcataaagtgaagaaccttttagagaagggcaacttgggttttcttctttagatcga 601  
DB 549 TTCATCAATGTAAGAAACATCTTTAGAGAGGCAATATCTTTGGTGTCTCTTGTGATCTA 608  
QY 602 ccaaaagtgaagaattccagtttgaacaacacagtgctccaataatggtcagaagataatg 661  
DB 609 CCAAAAGTGAAGATTCAGATTGTAACACACAGTGTCCAAATAATGTCAGAGATG 668  
QY 662 caggaataaataacatctctcaataatggtccttacttccgtgtgaaacctgac 721  
DB 669 CAGGAAAAAATTAACCATCTTCAATATAGTGTCTTAACTCCCGTGTGAAACCTGTATC 728  
QY 722 ctccacataataaaacctctctccacatgagtaacctatattgcaatggaggaatc 781

DB 729 CTCACATATTAAAAACCTCTCTCCACAGATGACCTATATGTCATGGGAGATC 788  
QY 782 cacaagaatttattagcagatgcctatttatagaagtagaagtaaacagccaaactg 841  
DB 789 CACAGAAATTTATTACAGATGCTTATTTATGAACTAAGTCAATTAACAGCAAACTG 848  
QY 842 agacacataatgttctcagct 863  
DB 849 AGACACATATGTTTCTACGT 870

RESULT 8  
LOCUS AF074402 1048 bp mRNA MAM 24-DEC-1998  
DEFINITION Bos taurus interleukin-13 receptor alpha-1 chain precursor, mRNA, partial cds.  
ACCESSION AF074402  
NID 94063012  
VERSION AF074402.1 GI:4063012  
KEYWORDS Bos taurus.  
SOURCE Bos taurus.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae;  
Bos.  
1. (bases 1 to 1048)  
AUTHORS Triгона, W.L., Hirano, A., Brown, W.C. and Estes, D.M.  
TITLE Biological activities of interleukin-13 on bovine lymphocytes:  
implications for signaling through IL-13Rα1  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1048)  
AUTHORS Triгона, W.L. and Estes, D.M.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-1998) Veterinary Pathobiology, University of  
Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO  
65211, USA

FEATURES  
source location/Qualifiers  
1..1048  
/organism="Bos taurus"  
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CDS  
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VRF"

BASE COUNT 321 a 227 c 216 g 284 t  
ORIGIN

Query Match 20.4%; Score 817.6; DB 3; Length 1048;  
Best Local Similarity 86.3%; Pred. No. 8e-192;  
Matches 904; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 136 gtgacaattgagtgctcgttgtaaaacctgcgcagcaagtaataatgagatgagatcca 195  
DB 1 GTGACAAATTTGAGTGTCTGTTGAAAACCTGTGACACATCATATGGACATGGAAATCCT 60  
QY 196 ccgagggagcagcagctcaaatgtgactatgagatattgagatatttggcgacaaacaa 255  
DB 61 COTGAGGAGCGACGACCAATTTGATGCTAAGTATTTCACTATTTTGGCAACAAACAG 120  
QY 256 gataagaataatgctcgggaacctcgtctcaatagagaatgacccctgaatgagagatt 315  
DB 121 GATAGAAAAATTTGCTCCAGAAACATCATGTTCAAAAAGAGTCCCTGTAACGAGAGATC 180



316 tctctcgaatgagggccagctgtagcaccatgagatgagaagccttagcttgc 375  
 181 tctctcgaatgagggccagctgtagcaccatgagatgagaagccttagcttgc 240  
 376 gaaatgcatcctcaccaccagagatgagctgagctgctgtagctgagcttgc 435  
 241 gaaatgcatcctcaccaccagagatgagctgagctgctgtagctgagcttgc 300  
 436 atttggcac 495  
 301 atttggcac 360  
 496 gac 555  
 361 gac 420  
 556 aacatctttag 615  
 421 aacttctttag 480  
 616 tccagctttag 675  
 481 tccagctttag 540  
 676 ccatctttag 735  
 541 ccatctttag 600  
 736 aacatctttag 795  
 601 aacttctttag 660  
 796 aacatctttag 855  
 661 aacttctttag 720  
 856 tctctcgaatgagggccagctgtagcaccatgagatgagaagccttagcttgc 915  
 721 tctctcgaatgagggccagctgtagcaccatgagatgagaagccttagcttgc 780  
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 781 aacttctttag 840  
 976 aacatctttag 1035  
 841 aacttctttag 900  
 1036 agatagtag 1095  
 901 agatagtag 960  
 1096 atcgtcgcag 1155  
 961 atcgtcgcag 1020  
 1156 tctctcgaatgagggccagctgtagcaccatgagatgagaagccttagcttgc 1183  
 1021 tctctcgaatgagggccagctgtagcaccatgagatgagaagccttagcttgc 1048

RESULT 9  
 LOCUS G29644 458 bp DNA STS 05-OCT-1996  
 DEFINITION human STS SHGC-34461, sequence tagged site.  
 ACCESSION G29644  
 NID 1593195  
 VERSION G29644.1 GI:1593195  
 KEYWORDS STS; STS sequence; primer; sequence tagged site.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE  
 1 (bases 1 to 458)  
 AUTHORS  
 MYERS, R.M.  
 JOURNAL  
 UNPUBLISHED (1996)  
 COMMENT  
 Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu

Primer A: TCTGTTATGCTTTGGGGG  
 Primer B: GAAATGCTCTCATTTCCCA  
 STS size: 128  
 PCR Profile:  
 Initial Incubation: 94 degrees C for 90 seconds  
 Denaturation: 94 degrees C for 15 seconds  
 Annealing: 62 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 Thermal Cycler: Perkin Elmer 9600

Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/uL  
 Total Vol: 10 uL  
 Buffer:  
 MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 80 mM  
 pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from R87164  
 -- Washington University/Merck EST sequence.

FEATURES  
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 /map="x"  
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 primer\_bind 23..42  
 primer\_bind complement(131..150)  
 BASE COUNT 111 a 103 c 110 g 128 t 6 others  
 ORIGIN

Query Match 7.0%; Score 281.8; DB 13; Length 458;  
 Best Local Similarity 96.6%; Pred. No. 1.6e-59;  
 Matches 310; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

2917 agcgaac 2976  
 6 agcgaac 65  
 2977 cctatccac 3036  
 66 cctatccac 125  
 3037 aagtagtag 3096  
 126 aactatgag 185  
 3097 attactgtag 3155  
 186 attactgtag 245  
 3156 ttatataatgag 3212

Db 246 TTAATACATGATGCTATTGCAATCTCTCTAGGAGGAGGAGATAGAAACC 305  
QY 3213 ctactctctacaggttg 3233  
Db 306 CTCACCTCTACAGGGTTGG 326

RESULT 10  
AC004824  
LOCUS AC004824 134578 bp DNA HTG 12-JUN-1998  
DEFINITION Homo sapiens clone D020B21, WORKING DRAFT SEQUENCE, 4 unordered  
pieces.  
ACCESSION AC004824  
NID 93213173  
VERSION AC004824.1 GI:3213173  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 134578)  
AUTHORS Waterston, R.H.  
JOURNAL The sequence of Homo sapiens clone  
Unpublished  
2 (bases 1 to 134578)  
AUTHORS Waterston, R.H.  
TITLE Submitted (12-JUN-1998) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
COMMENT \* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 6892: contig of 6892 bp in length  
\* 6909: gap of unknown length  
\* 17944: contig of 11035 bp in length  
\* 17961: gap of unknown length  
\* 17962: contig of 16558 bp in length  
\* 34520 34536: gap of unknown length  
\* 34537 134578: contig of 100042 bp in length.  
Location/Qualifiers  
1. 134578  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="D020B21"

BASE COUNT 32479 a 34383 c 33834 g 33831 t 51 others  
ORIGIN

Query Match 6.5%; Score 260; DB 33; Length 134578;  
Best Local Similarity 82.1%; Pred. No. 1.1e-53;  
Matches 299; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1816 ttaacagctggcgtggcgcgtgctacagcctgtaaccgaatttgagctcg 1875  
Db 11974 TTAGCTGGGCGAGGCTGGGGGCTGAGCTACGCTGTATATCCAGCACTTTGGAGGCG 12033

QY 1876 aggcgggcagatcactcgcagcagagttccagaccagcctgcagcaaaatgtgaacc 1935  
Db 12034 AGGTGGGCGAGTACACTGAGTTCAGAGATTGAGACCACTGGCCACATGTGAAACC 12093

QY 1936 tccctctactaataactcaaaatgaactggtgtgtgtgcgctgtgaatccag 1995  
Db 12094 CCGTCTCTACTTAAATAATCAAAATTAAGCTGGGCAATGTGTGAGGCTGTATATCCAG 12153

QY 1996 ctactcggaaactgagcaggtgaattgtgaacctggaggtggaggtgacgttg 2055  
Db 12154 CTACTCAGAGAGCTGAGGAGAGATTTGCTGTGAACTGTGGAGGCGAGGTGCAGTGTAG 12213

QY 2056 cagagatcacacactcgtacacttagcttggtgacagagcaagactctgtctaaaaaca 2115  
Db 12214 CCGAGATCACACCACTTGCACTTCAGGCTTGCGCTACAGAGCAAGACTCACTCAAAAAA 12273

QY 2116 aaacaaacaaacaaacaaacaaaccttaataattctgagatcatcctccctga 2175  
Db 12274 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTAGCTGGCATTATGTGTGCACTTG 12333

QY 2176 cagc 2179  
Db 12334 CAGC 12337

RESULT 11  
AC010532/c  
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SEQUENCE, 100 unordered pieces.  
ACCESSION AC010532  
NID 95882406  
VERSION AC010532.1 GI:5882406  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 141857)  
AUTHORS DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 16  
Unpublished  
2 (bases 1 to 141857)  
AUTHORS DOE Joint Genome Institute.  
TITLE Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
JOURNAL www.jgi.doe.gov  
COMMENT \* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 100 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 744: contig of 744 bp in length  
\* 745 gap of unknown length  
\* 1371: contig of 627 bp in length  
\* 1372 gap of unknown length  
\* 2098: contig of 727 bp in length  
\* 2099 gap of unknown length  
\* 2812: contig of 714 bp in length  
\* 2813 gap of unknown length  
\* 3460: contig of 648 bp in length  
\* 4008: contig of 548 bp in length  
\* 4009 gap of unknown length  
\* 4882: contig of 874 bp in length  
\* 4883 gap of unknown length  
\* 5597: contig of 715 bp in length  
\* 5598 gap of unknown length  
\* 6272: contig of 675 bp in length  
\* 6273 gap of unknown length  
\* 6993: contig of 721 bp in length  
\* 6994 gap of unknown length  
\* 7571: contig of 578 bp in length  
\* 7572 gap of unknown length  
\* 8247: contig of 676 bp in length  
\* 8248 gap of unknown length  
\* 8370: contig of 123 bp in length  
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\* 9493: contig of 1123 bp in length  
\* gap of unknown length

\* 9494 10046: contig of 553 bp in length  
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 \* 10047 11400: contig of 1354 bp in length  
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 \* 11401 12049: contig of 649 bp in length  
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 \* 12050 12626: contig of 577 bp in length  
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 \* 12627 13518: contig of 892 bp in length  
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 \* 13519 14325: contig of 807 bp in length  
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 \* 14326 15013: contig of 688 bp in length  
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 \* 16002 16602: contig of 601 bp in length  
 \* gap of unknown length  
 \* 16603 17537: contig of 935 bp in length  
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Query Match 6.3% Score 253.6; DB 42; Length 141857;  
 Best Local Similarity 84.1% Pred. No. 4,le-52;











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D	b	301	ctgaattgagagattttgtctcctcaagtggtgggtcccaagrtagaccacaatgaaagttagaag	360
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Qy	1801	gctattaacactctttaaacacgtcgtgcgtgggtccgggtgacacgccttaaccag	1860
Dh	1801	GCTATTAACACTCTTTTAACAGTCTGGGCTCGGTCGGTGCCTGTAATCCAG	1860
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Qy	1981	tgcctgttaatcccgacactccggaagcttgaagcagtgtaattgtttgaacctggaggt	2040
Dh	1981	TGCCGTGTAATCCGAGTACTCGGGAAGCTGAGCAGTGAATGTTGACTGGAGAGT	2040
Qy	2041	ggaggttgtagtgtagagagatacacacacttgacactctgacctgggtgtacagagcaag	2100
Dh	2041	GGAGGTTGACATGTGAGAGATATACACCACTGACACTGTGGGTGTGACAGAGCAACAC	2100
Qy	2101	tctctctaaaaaacaacaacaacaacaacaacaacaacacttataattcttggaggt	2160
Dh	2101	TCTCTCTAAAAAACAACAACAACAACAACAACAACAACAACCTTTATATTCTGAGGT	2160
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Dh	2161	CATCAATCCCTCTGACAGCAATTTCTCTGCTTTGAAGCCCAAAATACAGTGTGGCC	2220
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Qy	2281	tttagcctgtttagggcgagtggaagtgaatgacactcttggatattagagtttcaaccatg	2340
Dh	2281	TTTAGCTGTTAGGGCAGCTGAGAGTGAATGACTCCTTGATTAAGAGTTTCAACCATG	2340
Qy	2341	aagtccttaacaatgtaatttcttcaactctgctactcaagaatgacatttactgtgtctt	2400
Dh	2341	AAGTCCTTAACAATGTAATTTCTTCACTCTCTGACTCAAGTAGACATTTACTGTGTCTTT	2400



Qy	2401	ggtgtgcttagagcccccgggtgttgagaacagacccttcagggtttcaagcatt	2460
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Db	2461	TGAAGCTCTCAAGTCTTGTGCACCTTTTAAAACTCCACAGATCAATTTTCAGACT	2520
Qy	2521	tttaacctccaattccaacacatgattccccccttttgcaattccctccctccctcct	2580
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Db	2581	GTAACCTTTTGACTTTCATTGGAAATTAAGATGTAAATGTCTCAGAGACACTGGAGAG	2640
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Db	2641	CAGAGGAATTAATAGCATCTCAGGTCTAAGTGTAGTATCTGAGAAACATGACTAATCT	2700
Qy	2701	tgcgaatttggtaactcccatgtgagaggtttccagaattgatatttggcattttctaa	2760
Db	2701	TGCATATTTTGTACTTCCATGTGAGGGTTTCCGATTTGATTAATTTGTCAATTTCTAAA	2760
Qy	2761	cagaagatgagtgatccttcacatgtagaacatggtatcgtctgagaaaaaagaatag	2820
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Qy	2821	ttgaaactattctctctctctcttaagaagtggttccaagattccctcttctcgcataa	2880
Db	2821	TTGAACCTATTTCTCTTCTTCAAGATGGGTCAGGATTCCTCTTCTGTGCATAA	2880
Qy	2881	atgataatcaaatagcttttgcctcattggttagcagcagcagaagctcgtgt	2940
Db	2881	ATGATTAATTAATAGCTTTGTGTCTTCAATTGTGTAGGCACGACGACCAAGCTGTGTT	2940
Qy	2941	atgcttttggggggacataatctgggttccaactctcaactacacacaacataatccgat	3000
Db	2941	ATGCTTTTGGGGGGCATAATTTGGGTTCCATTTCCACTTCACATTCACACAACATATCCGAT	3000
Qy	3001	ataccccccttaccttacctccccccaattttaaagaagtatgggaaatgagaagccatt	3060
Db	3001	ATAATCCCTTACTCTTACTTCCCCCAAAATTAATTAAGATATGAGGAATGAGAGCATTT	3060
Qy	3061	ccccccaccatctctctctccacacacagactcatattactcgtgtagaacttgsaact	3120
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Qy	3121	ttaattccaagttgttcaaacatttccaatatataataaagatgactatttgcatt	3180
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Qy	3181	tcctgcctcccttagggaggggagaataagaaccctcaactctcacaagtttggtaagaat	3240
Db	3181	TCTGCTCTCTAGGGGAGGGAGATTAAGAAACCTCACTCTTCAAGGTTTGGGTGCAAGT	3240
Qy	3241	ggcaacctgcttccaatgagccgtgtagaagaatggtgacctgctctctgagaagctg	3300
Db	3241	GGCAACCTGCTTCCATGCGCGGTGAAGATGTGTCCCTGCTTCTCTGAGGAAGCTGG	3300
Qy	3301	ggttcacagcaatgagcagatgtaagtttactcttgaaagcagaattgagagctgggagag	3360
Db	3301	GGTTCATGACAAATGGCAGATGTAAAGTTATCTTGAAAGTCAATTTGAGGCTGGAGAGAG	3360
Qy	3361	ccgtagtagaagtctcaacttgttctcgtgttctctagaagaataattggtttctcgt	3420
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Qy	3421	atagaagatgagataattcccttccagagatttataaattcctgggaaacaaaccatcgc	3480
Db	3421	ATAGAATGAGATTAATTTCTTCTTCCAGGATTTTATTAATTTCTGGGAAGAAAACCATATGC	3480

Accession	Gene	Protein	Length	Start	End	Score	E-value	Ident	Positives	Negatives	Gap	Frames	Conserved	Conserved2	Conserved3	Conserved4	Conserved5	Conserved6	Conserved7	Conserved8	Conserved9	Conserved10	Conserved11	Conserved12	Conserved13	Conserved14	Conserved15	Conserved16	Conserved17	Conserved18	Conserved19	Conserved20	Conserved21	Conserved22	Conserved23	Conserved24	Conserved25	Conserved26	Conserved27	Conserved28	Conserved29	Conserved30	Conserved31	Conserved32	Conserved33	Conserved34	Conserved35	Conserved36	Conserved37	Conserved38	Conserved39	Conserved40	Conserved41	Conserved42	Conserved43	Conserved44	Conserved45	Conserved46	Conserved47	Conserved48	Conserved49	Conserved50	Conserved51	Conserved52	Conserved53	Conserved54	Conserved55	Conserved56	Conserved57	Conserved58	Conserved59	Conserved60	Conserved61	Conserved62	Conserved63	Conserved64	Conserved65	Conserved66	Conserved67	Conserved68	Conserved69	Conserved70	Conserved71	Conserved72	Conserved73	Conserved74	Conserved75	Conserved76	Conserved77	Conserved78	Conserved79	Conserved80	Conserved81	Conserved82	Conserved83	Conserved84	Conserved85	Conserved86	Conserved87	Conserved88	Conserved89	Conserved90	Conserved91	Conserved92	Conserved93	Conserved94	Conserved95	Conserved96	Conserved97	Conserved98	Conserved99	Conserved100	Conserved101	Conserved102	Conserved103	Conserved104	Conserved105	Conserved106	Conserved107	Conserved108	Conserved109	Conserved110	Conserved111	Conserved112	Conserved113	Conserved114	Conserved115	Conserved116	Conserved117	Conserved118	Conserved119	Conserved120	Conserved121	Conserved122	Conserved123	Conserved124	Conserved125	Conserved126	Conserved127	Conserved128	Conserved129	Conserved130	Conserved131	Conserved132	Conserved133	Conserved134	Conserved135	Conserved136	Conserved137	Conserved138	Conserved139	Conserved140	Conserved141	Conserved142	Conserved143	Conserved144	Conserved145	Conserved146	Conserved147	Conserved148	Conserved149	Conserved150	Conserved151	Conserved152	Conserved153	Conserved154	Conserved155	Conserved156	Conserved157	Conserved158	Conserved159	Conserved160	Conserved161	Conserved162	Conserved163	Conserved164	Conserved165	Conserved166	Conserved167	Conserved168	Conserved169	Conserved170	Conserved171	Conserved172	Conserved173	Conserved174	Conserved175	Conserved176	Conserved177	Conserved178	Conserved179	Conserved180	Conserved181	Conserved182	Conserved183	Conserved184	Conserved185	Conserved186	Conserved187	Conserved188	Conserved189	Conserved190	Conserved191	Conserved192	Conserved193	Conserved194	Conserved195	Conserved196	Conserved197	Conserved198	Conserved199	Conserved200	Conserved201	Conserved202	Conserved203	Conserved204	Conserved205	Conserved206	Conserved207	Conserved208	Conserved209	Conserved210	Conserved211	Conserved212	Conserved213	Conserved214	Conserved215	Conserved216	Conserved217	Conserved218	Conserved219	Conserved220	Conserved221	Conserved222	Conserved223	Conserved224	Conserved225	Conserved226	Conserved227	Conserved228	Conserved229	Conserved230	Conserved231	Conserved232	Conserved233	Conserved234	Conserved235	Conserved236	Conserved237	Conserved238	Conserved239	Conserved240	Conserved241	Conserved242	Conserved243	Conserved244	Conserved245	Conserved246	Conserved247	Conserved248	Conserved249	Conserved250	Conserved251	Conserved252	Conserved253	Conserved254	Conserved255	Conserved256	Conserved257	Conserved258	Conserved259	Conserved260	Conserved261	Conserved262	Conserved263	Conserved264	Conserved265	Conserved266	Conserved267	Conserved268	Conserved269	Conserved270	Conserved271	Conserved272	Conserved273	Conserved274	Conserved275	Conserved276	Conserved277	Conserved278	Conserved279	Conserved280	Conserved281	Conserved282	Conserved283	Conserved284	Conserved285	Conserved286	Conserved287	Conserved288	Conserved289	Conserved290	Conserved291	Conserved292	Conserved293	Conserved294	Conserved295	Conserved296	Conserved297	Conserved298	Conserved299	Conserved300	Conserved301	Conserved302	Conserved303	Conserved304	Conserved305	Conserved306	Conserved307	Conserved308	Conserved309	Conserved310	Conserved311	Conserved312	Conserved313	Conserved314	Conserved315	Conserved316	Conserved317	Conserved318	Conserved319	Conserved320	Conserved321	Conserved322	Conserved323	Conserved324	Conserved325	Conserved326	Conserved327	Conserved328	Conserved329	Conserved330	Conserved331	Conserved332	Conserved333	Conserved334	Conserved335	Conserved336	Conserved337	Conserved338	Conserved339	Conserved340	Conserved341	Conserved342	Conserved343	Conserved344	Conserved345	Conserved346	Conserved347	Conserved348	Conserved349	Conserved350	Conserved351	Conserved352	Conserved353	Conserved354	Conserved355	Conserved356	Conserved357	Conserved358	Conserved359	Conserved360	Conserved361	Conserved362	Conserved363	Conserved364	Conserved365	Conserved366	Conserved367	Conserved368	Conserved369	Conserved370	Conserved371	Conserved372	Conserved37
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CC availability of genetic sequences for NR4 permits the development  
 CC of a range of agents capable of modulating the activity of IL-13  
 CC and related cytokines such as interleukin-4 for the treatment of  
 CC allergy, asthma and other conditions relating to IgE. The genetic  
 CC sequences can also be used in prodn. of recombinant NR4 or fusion  
 CC proteins including NR4.  
 SQ Sequence 1383 BP; 421 A; 292 C; 319 G; 351 T;

Query Match 33.3%; Score 1333.8; DB 1; Length 1383;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

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QY 7 cggcggcgcccgaggagagagctgcatgagtgccgagcgctcgtcgagctcgtgag 66
Db 34 CGGCGGGGTTCCGAGGAGGAGGCTCATGAGTGGCGGCGGGGCTCGCGGGCTGTGG 93
QY 67 ggcgtcgtctcgtcgccgagcgagcgagcgagcgagcgagcgagcgagcgagc 126
Db 94 GCGCTGCTGCTGCGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGG 150
QY 127 cagccacccgtgacaaattgagtgctcgtctgttgaacacctcgcacagtaataagaca 186
Db 151 CAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTGCGACAGTAATGAGACA 210
QY 187 tggatccaccccgagggagccagctcaattgtagtctatgtatgtatgtatgtatgt 246
Db 211 TGGAAATCCACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 270
QY 247 gacaaacagataaagaatagctccggaacacctgcttcaatagaagtaaccctgaat 306
Db 271 GACAAACAGATAGAAATAGCTCCGGAACCTGCTGTTCAATAGAAATACCCCTGAAT 330
QY 307 gaggagatttctcgaagtgagtgccagtgtagcacaataagaagtgagaagcttagc 366
Db 331 GAGAGGATTTGTCGAAATGGGGTCCAGTGTAGACCAATAGAGTGAAGAGCTTAC 390
QY 367 atttgggtgaaataatgacatcaccaccccgagagtgatcctcgtcgtcgtcgtcgt 426
Db 391 ATTTGGTGTGAAAATGATCATCTACCCCGAAGAGTGATGCTGAGTCTGCTGCTGAA 450
QY 427 ctccatgctcgttggcacaacctgagctacatgaagtgcttgcctcgtcgtcgtcgtcgt 486
Db 451 CTTCAATGCTTTGGGACACACCTGACCTACATGAGTGTCTTGGCTCCCTGGAGGAGAT 510
QY 487 accagtcgccgacacatactatcttactatcttggcagaagccttgaaaaaatcat 546
Db 511 ACCAGTCCCGACACTATCTCTCTACTATTGGCAGACAGCCTGGAATAATTCAT 570
QY 547 caatlgaaaaacattttagaagaagccaacttctgttcttcttcttcttcttcttct 606
Db 571 CAATGTGAAACATCTTTAGAGAGGCCAATCTTGGTTCTTCTTCTTCTTCTTCTTCT 630
QY 607 gtgaagagatccagttttagaacaacacagtgctcaataaatgylcaagaataatgacag 666
Db 631 GTGAAGGATTCAGTTTGAACAAACAGTGTCAATAATATGTCGAAGATATGACGGA 690
QY 667 aaattaaacacatcttcaatataatagtgcttcaactcccggttgaaaacctgtctca 726
Db 691 AAAATTAACCATCTTCAATATAGTCCCTTAACTTCCGCTGTGAACCTGATCTCTCA 750
QY 727 catattaaaacctctctccacaatgatgactatagtgcaatgggagagatccacag 786
Db 751 CATATTAAAAACCTCTCTCCACATGATGACCTATATGTGCAATGGGAGAACTCACAG 810
QY 787 aatttatgtgagatgagctatttttagaagtagaagtgcaataaagaacaaacttgagca 846
Db 811 AATTTATTATGACGATGCCATTTTATGAGTAGAAGTCAATTAAGCCAAACTGAGACA 870
QY 847 cataatgtttctacgtccagaagagtaattgtgaatccagaatgttgaagaatgtg 906
Db 871 CATTAATGTTTCTAGTCCAGAGGCTTAATAGTGAATCCAGATTTGAGAGAAATGTG 930

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QY 907 gagaatcatcttcttcaatgagtgccctggtgtctctccgatacttgaacacagtcaga 966
Db 931 GAGATATCATCTTTTCATGTCGCCCTGGTGTCTTCTGATCTTGAACACAGTCAGA 990
QY 967 ataagatcaaaaaaataaagtatgatatagagatgaacaaactctgagatattgagac 1026
Db 991 ATNAGATCAAAACAAATATGATGATGATGAGGATGAGGATGAGGATGAGGATGAGG 1050
QY 1027 caagaatagatagtagtaagaagcgcaattccacacttacaataacatgttactca 1086
Db 1051 CAAGAAATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1110
QY 1087 gtccagatagtgtagcagagtgcaatcagtagtaccctgtcttcaactaagaagctaa 1146
Db 1111 GTTCCAGTATGTCGACAGTGCATATGATGATGATGATGATGATGATGATGATGAT 1170
QY 1147 attatatttccctcccaattccctgacccctgcaagatttttaagaatgttggagac 1206
Db 1171 ATTATTATTTTCCCAATTCCTGATCTTGCAGAGATTTTAAAGAAATGTTGGAGAC 1230
QY 1207 cagaatgtagtactctgacactggaagaagtagacatcatgagaagcaaaccaagag 1266
Db 1231 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1290
QY 1267 gaacgcactctgtagtgctgtagtaagaacactgaagaagccctcagtgatgagata 1326
Db 1291 GAAACCGACTGTAGTGTGATGAGAAACCTGAGAGAAAGCCCTGAGTGTGAGATTA 1350
QY 1327 ttatttttacttactcactgagccttgagaaga 1359
Db 1351 TTTATTTTACCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383

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RESULT 3  
 T66164  
 ID T66164 standard; DNA; 1383 BP.  
 AC T66164;  
 DT 15-JUL-1997 (first entry)  
 DE Mouse Interleukin-12 receptor alpha chain NR4 DNA.  
 KW haemopoietin receptor; Interleukin-13 receptor; IL-13;  
 OS Mus sp.  
 FX Key Location/Qualifiers  
 FT cds 61..1341  
 FT signal\_peptide 61..141  
 FT mat\_peptide 142..1338  
 FT misc\_difference 121..123  
 FT /tag- d /note- "bases 121-123 (unn) code for an unidentified amino acid"  
 FT /tag- e /note- "bases 640-642 (unn) code for an unidentified amino acid"  
 FT /tag- e /note- "bases 640-642 (unn) code for an unidentified amino acid"  
 FT W09715663-A1.  
 FT 01-MAY-1997.  
 FT 23-OCT-1996; AU0668.  
 FT 23-OCT-1995; AU-006135.  
 FT 22-DEC-1995; AU-007276.  
 FT 09-SEP-1996; AU-002208.  
 FT (AMLA-) AMRAD OPERATIONS PTY LTD.  
 FT HILTON DJ Metcalfe D, Nicola NA, Willson T, Zhang JG;  
 FT WPI: 97-258018/23.  
 FT P-PSDB: W09821.  
 FT DNA encoding animal haemopoietin receptor which interacts with  
 FT Interleukin-13 - useful to treat asthma, allergy or condition  
 FT Claim 6; Page 48-50; 93pp; English.  
 CC DNA sequences (T66164 and T66165) respectively code for novel mouse  
 CC and human haemopoietin receptors (W09821 and W09822) designated NR4



CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal  
 CC infections, for autoimmune diseases such as multiple sclerosis or  
 CC systemic lupus erythematosus, to regulate hematopoiesis, for tissue  
 CC growth, as an activator or inhibitor, or as a chemotactic or  
 CC chemokinetic, haemostatic and thrombocytic, receptor/ligand, or  
 CC anti-inflammatory or tumour inhibitor agents.  
 SO Sequence 592 BP; 197 A; 121 C; 105 G; 169 T;

Query Match 14.8%; Score 592; DB 1; Length 592;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-136;  
 Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 ttgttccttgcattgcacaaagtgaaagatccagtttgtaacacacagtcgccaat 644  
 DB 1 ttgttccttgcattgcacaaagtgaaagatccagtttgtaacacacagtcgccaat 60  
 QY 645 aatgtcaagataatgagagaaataaaccatcccttaataatagtccttaattc 704  
 DB 61 AATGCTCAAGATATGAGAGAAATTAACCATCCCTCAATATAGTGCCTTAACCTC 120  
 QY 705 ccgtgtgaacatgcctccacataataaaacctctctccacacatgagcctata 764  
 DB 121 CCGGTGTAACCTGATCCTCCACATATTAACCTCTCTCCACATATGAGCCTATA 180  
 QY 765 ttgtcaatgagagatccacagaaatttattagacagatgctatttattagaaagat 824  
 DB 181 TGTCGAATGGAGATCCACAGATTTATTAGCAGATGCCCTATTATTAGAGTAGAGT 240  
 QY 825 caataacagcaaacctagacacataatgtttctagctcaagagagctaaatgagaa 884  
 DB 241 CAATTAACAGCAACCTAGACACATATGTTTCTACGTCCAAAGGCTAAAGTAGAGA 300  
 QY 885 tccagaattgagagaaatgtgagaaatacatctgtttcaatggtccgtgtctcc 944  
 DB 301 TCCGATTTGAGAGAAATGTGAGATACATCTTTTCATGTCCTCCGTGTTCTTCC 360  
 QY 945 tgaactttgaacacagtcagcaataagagtcacaaacaaataagttatgtatagagaga 1004  
 DB 361 TGATACTTTGAACACAGTCGATGATTAAGAGTCACAAACAAATTAAGTATGAGAGATGA 420  
 QY 1005 caaaccttgagtaattgtgagccaagaataatgagtagagaaagcgcgaattccacact 1064  
 DB 421 CAAACCTGTGAGTAATTTGAGCCAAAGAAATGAGTATAGTAAGAGCCGAATTCACACT 480  
 QY 1065 ctacataacacatgttactatgttccagtcactgcgcaggtgcacatagtaactcct 1124  
 DB 481 CTACATAACCATGTTACTATGTTCCAGTCATCGTCGAGGTGCATCATAGTACTCCT 540  
 QY 1125 gcttaactaaaggctcaagatatattatccctcaattcctgactcct 1176  
 DB 541 GCTTACCTAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATCCT 592

RESULT 5  
 V89658  
 ID V89658 standard; cDNA; 391 BP.  
 AC V89658;  
 DT 15-FEB-1999 (first entry)  
 DE EST clone DA136.  
 KW Human; secreted protein; expressed sequence tag; EST; hematopoiesis;  
 KW tissue growth; activin; inhibitor; chemotaxis; chemokinesis; haemostatic;  
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;  
 KW gene therapy; ss.  
 OS Homo sapiens.  
 PN WO9845436-A2.  
 PD 15-OCT-1998.  
 PF 10-APR-1998: US-69555.  
 PR 10-APR-1997: US-838821.  
 PA (GENE) GENETICS INST INC.  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,  
 PI Racie LA, Spaulding V, Treacy M;  
 ER WPI; 99-07007/06.

PT New polynucleotides encoding human secreted proteins - derived from  
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,  
 PT ovary, pituitary, retina and colon cDNA libraries.  
 PS Claim 1: Page 288, 618pp; English.

CC The present sequence represents a human expressed sequence tag (EST).  
 CC The polynucleotide, which is a secreted EST, and the encoded protein  
 CC are predicted to have useful biological activities which would make  
 CC them suitable for treating, preventing or ameliorating medical  
 CC conditions in humans and animals, although no supporting data is  
 CC given. Suggested activities include nutritional activity, immune  
 CC stimulating or suppressing activity, haematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic  
 CC activity, receptor/ligand activity, anti-inflammatory activity,  
 CC cadherin/tumour invasion suppressor activity, tumour inhibition  
 CC activity. The polynucleotide may also be useful for gene therapy.  
 SO Sequence 391 BP; 127 A; 82 C; 75 G; 107 T;

Query Match 9.0%; Score 360.8; DB 1; Length 391;  
 Best Local Similarity 99.5%; Pred. NO. 9.8e-80;  
 Matches 362; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 824 tcaataacagcaaacctagacacataatgtttctacgtccacagagctaaatgtaga 883  
 DB 24 TCAATTAACGCCAACTAGACACATATGTTTCTACGTCCAAAGGCTAAAGTAGAGA 83  
 QY 884 atccagaattgagagaaatgagagatacatctgtttcaatggtccgtgtcttc 943  
 DB 84 ATCCGAAATTTGAGAGAAATGTGAGAAATCATCTTTTCATAGTCCGAGTCTTCC 143  
 QY 944 ctgatactttgaacacagtcagcaataagagtcacaaacaaataagttatgtaagagatg 1003  
 DB 144 CTGATCTTTGAACACAGTCGATGATTAAGAGTCACAAACAAATTAAGTATGCTATGAGAGATG 203  
 QY 1004 acaaaccttgagtaattgtgagccaagaataatgagtagagtagagaaagcgcaattccacac 1063  
 DB 204 ACAACCTGTGAGTAATTTGAGCCAAAGAAATGAGTATAGTAAGAGCCGAATTCACACT 263  
 QY 1064 tctacataacacatgttactatgttccagtcactgcgcaggtgcacatagtaactcct 1123  
 DB 264 CTACATAACCATGTTACTATGTTCCAGTCATCGTCGAGGTGCATCATAGTACTCCTC 323  
 QY 1124 tgccttaaccataaaggctcaagatatattatccctcaattcctgactcctgagaga 1183  
 DB 324 TGCCTTACCTAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATTCGCAAGA 383  
 QY 1184 ttct 1187  
 DB 384 ATCT 387

RESULT 6  
 V11621  
 ID V11621 standard; cDNA; 340 BP.  
 AC V11621;  
 DT 11-SEP-1998 (first entry)  
 DE Homo sapiens adult placenta clone DA136.11 5' region.  
 KW adult; placenta; cDNA library; clone DA136.11; anti-inflammatory;  
 KW therapeutic composition; autoimmune disease; immune; stimulation;  
 KW suppression; ds.  
 OS Homo sapiens.  
 PN WO9814576-A2.  
 PD 09-APR-1998.  
 PF 03-OCT-1997: U18007.  
 PR 04-OCT-1996: US-726237.  
 PA (GENE) GENETICS INST INC.  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,  
 PI Racie LA, Spaulding V, Treacy M;  
 DR WPI; 98-240082/21.  
 PT Nucleic acids encoding novel secreted proteins - useful as, e.g.  
 PT anti-inflammatory, immuno-stimulatory or suppressing agents  
 PS Claim 45; Page 80; 110pp; English.

CC The sequence is that of an isolated polynucleotide which may  
 CC be of use in the production of therapeutic compositions for  
 CC treating or ameliorating a medical condition in a mammal. Such  
 CC compositions may be used for, e.g. research purposes as markers for  
 CC tissues, molecular weight markers for gels, primers or probes, for  
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be  
 CC used as a cytokine for cell proliferation and differentiation activity,  
 CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal  
 CC infections, for autoimmune diseases such as multiple sclerosis or  
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue  
 CC growth, as an activator or inhibitor, or as a chemotactic or  
 CC chemokinetic, haemostatic and thrombocytic, receptor/ligand,  
 CC anti-inflammatory or tumour inhibitor agents.  
 SO Sequence 340 BP; 101 A; 73 C; 79 G; 85 T;

Query Match 8.4%; Score 336.4; DB 1; Length 340;  
 Best Local Similarity 99.1%; Pred. No. 9.4e-74;  
 Matches 337; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0Y 120 ggaactcagccacccctgtacaaattgtgtctctgttgaacctctgcagtaatt 179  
 DB 1 GGAACCTCACCACCTGTACAAATTGAGTGTCTGTGAAACCTGCACAGTAAT 60  
 0Y 180 atgagacatgaaatccacccagagagagcagctcaaatgttagctatgtattagta 239  
 DB 61 ATGAGACATGAAATCCACCCGAGAGAGCCAGCTCAATGTAGCTATGATTTAGTCA 120  
 0Y 240 ttctggcagcaaaacagaataagaataatagctccggaactcgtcgttcaatagaatcc 299  
 DB 121 TTTTGGCGCAACAAGATAAGAAATAGCTCCGGAACCTCGTCAATAGAAATAC 180  
 0Y 300 cctgaatagagagattgtctcgaagtgggtccagcttagacaaatagaataga 359  
 DB 181 CCGTAATGAGAGATTGTCTGCAAGTGGGTCCAGGTATACCAATAGAGAGTGA 240  
 0Y 360 gcttagcatcttgttgaataatgcatccaccaccagagaagtgatcctgaatcgt 419  
 DB 241 GCTTAGCATTTGTGTTGAAATAATGATCTCACCCAGAGAGGATCGTAATCTCTGT 300  
 0Y 420 gactgaagctcaatgcatttgcacaaactgagctacatg 459  
 DB 301 GACTGAGCTTCAATGATTTGGCACAACTGAGCTACATG 340

## RESULT 7

AC 11-SEP-1998 (first entry)  
 DE Homo sapiens adult placenta clone DA136.11.3' region.  
 KW adult; placenta; cDNA library; clone DA136.11; anti-inflammatory;  
 KW therapeutic composition; autoimmune disease; immune; stimulation;  
 OS Homo sapiens.  
 PN WO9814576-A2.  
 PD 09-APR-1998.  
 PF 03-OCT-1997.  
 PR 04-OCT-1996; US-726237.  
 PA (GENY) GENETICS INST INC.  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Werberg D,  
 PI Racine LA, Spaulding V, Treacy M;  
 DR MPI: 98-240082/21.  
 PT Nucleic acids encoding novel secreted proteins - useful as, e.g.  
 PT anti-inflammatory, immuno-stimulatory or suppressing agents  
 PS Claim 45; Page 82; 110p; English.  
 CC The sequence is that of an isolated polynucleotide which may  
 CC be of use in the production of therapeutic compositions for  
 CC treating or ameliorating a medical condition in a mammal. Such  
 CC compositions may be used for, e.g. research purposes as markers for  
 CC tissues, molecular weight markers for gels, primers or probes, for  
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be  
 CC used as a cytokine for cell proliferation and differentiation activity,

CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal  
 CC infections, for autoimmune diseases such as multiple sclerosis or  
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue  
 CC growth, as an activator or inhibitor, or as a chemotactic or  
 CC chemokinetic, haemostatic and thrombocytic, receptor/ligand,  
 CC anti-inflammatory or tumour inhibitor agents.  
 SO Sequence 285 BP; 93 A; 36 C; 50 G; 98 T;

Query Match 6.4%; Score 258.4; DB 1; Length 285;  
 Best Local Similarity 96.6%; Pred. No. 1.4e-54;  
 Matches 259; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

0Y 3742 tctgggaattagtaggcaattactgttttaggtcagcagcttgatgtttcccta 3801  
 DB 1 TGTGGAAATTTAGTAGGCTCATTTACTGTTTTAGGCTTACGATATGATTTTCCCTA 60  
 0Y 3802 acatacctaagcaaacccagctcagagatgtaattcttattcttcgtcagtaagt 3861  
 DB 61 ACATACCTAAGCAACCCAGNGTCAGATGAGNATTTATTCTTTCGTTCACTTAAGTT 120  
 0Y 3862 ttcccttcaatcggcagcactgaaagagatatgaaacaatgttaacatttggtagct 3921  
 DB 121 TTTCCTTTATNNGGCGCACTGAAGGATATGTAAACAATGTTTACATTTTGTGTT 180  
 0Y 3922 tccacagagattgttctcgttacttctttagaagaagcttgagtaataaatatg 3981  
 DB 181 TCACACCGGATTTGTTCTGTTTAATCTTTATAGAAACCTTGATTAATAATATTTG 240  
 0Y 3982 tcttttgcattgcacccaataaaaaa 4039  
 DB 241 TCTTTTGTATGTACACCAAAAAA 268

## RESULT 8

ID T22947 standard; cDNA to mRNA; 265 BP.  
 AC T22947;  
 DT 24-OCT-1996 (first entry)  
 DE Human gene signature HMG504672.  
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; ss.  
 OS Homo sapiens.  
 PN WO9514772-A1.  
 PD 01-JUN-1995.  
 PF 11-NOV-1994; J01916.  
 PA 13-NOV-1993; JP-355504.  
 PA (MATS/) MATSUBARA K.  
 PA (OKUB/) OKUBO K.  
 FI Matsubara K, Okubo K;  
 DR MPI: 95-206931/27.  
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that  
 PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues  
 PS Claim 1; Page 1252; 2245pp; Japanese.  
 CC A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
 CC given in T19001-726837 and which is able to hybridise to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.  
 SO Sequence 265 BP; 56 A; 50 C; 59 G; 91 T;

RESULT 9

V55039/C  
ID V55039; standard; cDNA; 6669 bp.  
AC V55039;  
DT 13-NOV-1998 (first entry)  
DE Human HIAP-1 coding sequence.  
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAY polypeptide;  
KW Proliferative disease; IAP therapy; cancer; human; HIAP-1 protein; ss  
KW Homo sapiens.  
FT Key  
FT Location/Qualifiers  
CD5 4221..6035  
          /\*tag= a  
          /product= HIAP-1

W09835693.A2  
70-RJ2895.CD

PF 20-AUG-1998.  
 PR 13-FEB-1998; 1B0781.  
 PR 13-FEB-1997; US-800929.  
 PA (UYOT-) UNIV. OTTAWA.  
 PI Baird S., Korneluk R., Liston P., Mackenzie AE, Pratt C,  
 PI Tsang B.,  
 DR WPI: 98-467164/40.  
 P-PDSB: W69295.  
 PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
 PT of IAP or NAIP polypeptide - also methods for prognosis based on  
 PT presence of IAP and NAIP, specifically applied to cancers involving  
 PT p53 mutations  
 PS Claim 13; Fig 2; 147Pp; English.  
 CC This sequence encodes the human HIAP-1 protein, which is a inhibitor of  
 CC apoptosis protein (IAP), and can be used in the method of the invention.  
 CC The method is for enhancing apoptosis in cells from a mammal with  
 CC proliferative disease by treatment with a compound that inhibits  
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
 CC compounds are used to treat proliferative diseases. The inhibitory  
 CC compounds are used to treat proliferative diseases, specially cancers of  
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
 CC rectum, cervix or endometrium, particularly to increase their sensitivity  
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
 CC detected in many cancers and are associated with poor prognosis,  
 CC suggested that chemotherapeutic agents and mutations in p53 (it is  
 CC genes). Transgenic animals are used for testing the effects of the IAP or NAIP  
 CC oligonucleotides and for screening for the inhibitors  
 SQ Sequence 6663 Bp. 2167 A; 1134 C; 1257 G. 2000-

Query Match 6.08; Score 239.6; DB 1; Length 6669

Best Local Similarity 84.6%; Pred. No. 2.4e-49  
Matches ~ 269; Conservative 0; Mismatches 4

		Indels	Gaps
QY	1822 gtttgagcgcggggtccggtgagctcaacgcctgtatccccaagaatttggagtcgcgaagcg	1881	
Db	1370 GCCTTCGCTGTGTGAGAGGCTCAGCGCTGTAAATCCAGCATTTTGGAGGCCAAGACAA	1311	
QY	1882 gcgatcatctcaggttcagagagttccagacagcgcctgagaccaaaatggtgaacctctct	1941	
Db	1310 GTGGATATCTTTGAGTGCAGAGCTTCATAACCGAGCTTGGCCAAATGCTGAATCCCATCT	1251	
QY	1942 ctacctaactactaaaaaattaaactcgggtgtgtgtgcgcctgacctgaatcccaagctatct	2001	
DJ	1250 CTACTATAAATAATCAAAAAATTAGCTGGGCTGTGTGTGATCGCGCTTAATCCAGCTTACT	1191	
QY	2003 gggaaagctcgagcgcaggtgtaattgtttgaacctgggaagtggaaggttcagtgacagaga	2061	
Dh	1190 GCGAGCGTGCAGGCGAGCGAGATTCATTGTAACCTCGGAGGCTGGAGGTGCAGTGGGCGCAAA	1131	
QY	2062 tcaaccaactcgcactctaaagccttgggtgtaacagagcaagaactcgtcttaaaaaacaacaa	2121	
DJ	1130 TAGTGCCACATACACTCCAGCGCTGGGTGAGACACGAAAGACTGTGTCTCAAAAATTAATTA	1071	
QY	2122 aacaaaacaaatacaaaaaa 2139		
Dp	1070 AATAAATAATAAACCCACGA 1053		

RESULT	10
V35620	

ID V35620 standard; DNA: 32367 BP.  
AC V35620;  
DC 07-SEP-1998 (first entry)  
DE Human SHOX (short stature homeobox containing gene) gene sequence.  
KE Homeobox domain; human growth gene; growth regulation; growth defect;  
KW Turner's syndrome; short stature homeobox containing gene; SHOX;  
KM SHOX: bone disease; osteoporosis; calcium regulation; short stature;  
KK transcription factor A; ss.  
OS Homo sapiens.  
PN M09814568-A1.  
PD 09-APR-1998.  
PE 29-SEP-1997; E05355.  
PR 16-JAN-1997; EP-100583.  
PR 01-OCT-1996; US-027633.  
PA (RAPF.) RAPFOLD-HOEKBRAND G.  
PI Rao E, Rapold-Hoerstrand G;  
DR APL 98-21719/24.  
PM New human growth genes - used to develop products for the diagnosis  
P1 and treatment of human growth defects such as short stature, e.g.  
PS Turner's syndrome  
PT Claim 19; Pages 51-67; 84pp. English.  
CC This is the human SHOX gene sequence containing the PARI region. The gene  
CC region corresponding to short stature has been identified as a region of  
CC approximately 500 kb in the PARI region of the X and Y chromosomes. Three  
CC genes in this region have been identified as candidates for the short  
CC stature gene. These genes were designated SHOX (also referred to as  
CC SHOX93 or HOX93), PTF92 and SHOT (SHOX-like homeobox gene on chromosome  
CC three). The SHOX gene has two separate splicing sites resulting in two  
CC variations SHOXA and SHOXB. The specification provides sequences of SHOX  
CC (short stature homeobox-containing) genes SHOX ET92, SHOXA, SHOXB, SHOT  
CC and exons of the SHOX genes as shown in V35610 to V35621 and protein  
CC and SHOT as shown W60573 to W60575. The novel genes are responsible for  
CC human growth. Defects in the genes can cause short stature, e.g.  
CC Turner's syndrome. The products can be used to develop agents for the  
CC treatment of short stature or other human growth disorders. The products  
CC can also be used for providing a mitogenic effect on cells, e.g. for the  
CC treatment of bone diseases such as osteoporosis and diseases involved  
CC with disturbance in the bone calcium regulation.  
SQ Sequence 32367 BP: 7627 A; 8130 C; 8564 G; 8973 T

6.08; Score 239; DB 1; Length 32367



CC CT stature gene. These genes were designated SHOX (also referred to as  
CT SHOX3 or FOX93), PTH92 and SHOT (SHOX-like homeobox gene on chromosome  
CC 17p13). The SHOX gene has two separate splicing sites resulting in two  
CC three) isoforms, SHOXA and SHOXB. The specification provides sequences of SHOX  
CC variations, SHOXA and SHOXB. The specification provides sequences of SHOX  
CC (short stature homeobox-containing) genes SHOX E792, SHOXA, SHOXB, SHOT  
CC and exons of the SHOX genes as shown in V35610 to V35621 and protein  
CC sequences of the human growth protein transcription factor SHOXA, SHOXB,  
CC C3 and SHOT are shown M60573 to M60575. The novel genes are responsible for  
CC human growth defects. Defects in the genes can cause short stature, e.g.  
CC Turner's syndrome. The products can be used to develop agents for the  
CC treatment of short stature or other human growth disorders. The product  
CC can also be used for providing a mitogenic effect on cells, e.g. for the  
CC treatment of bone diseases such as osteoporosis and diseases involved  
CC with disturbance in the bone calcium regulation.

SQ Sequence 15577 BP; 3692 A; 3875 C; 4196 G; 3629 T;

Query Match 5.9%; Score 237.4; DB 1; Length 15577;  
Fast Local Similarity 81.8%; Pred. No. 1.2e-48;  
Matches 274; Conservative 0; Mismatches 61; Indels 0; Gaps

DY 1807 aaacactttaacaagctcggcggtggtgcgttgctcacgcttcaatccagcaattt 1866  
|||  
DB 10659 AAACCCAAATTTCCAGTTCAGGCGCCAGGTGCAGTGACTGCATCCCACTTT 10718  
|||  
DY 1867 gggaagtcaggagggggggcgagatcatcccgggggtcagaagtccaagcccgcttgaccaaat 1926  
|||||  
DB 10719 GGGAAGGCCCAAGGAGGGTGGATGCTTGAGGTGAGAGAGTGCAGACCGCCTGCCAACAT 10778  
|||||  
DY 1927 ggtgaaccctccctctactaaactataaaaattaagtgggtgtgtgtgcggtcctgt 1986  
|||  
DB 10779 GGTGAACCACCCCACTTTACTATAAATTACAACAGTTAGTGGGTGTGTTGTTGCCCTG 10833  
|||||  
DY 1987 taatcccaactctacgcgggaagcttgaggaagtgtaattgtttgaacctggaaggttggaagt 2046  
|||  
DB 10839 TAATCCAGTACTCTCGGAAGTGTGAGGTGAGGTAATGCTTGAAATCTGGAGGTGAGGT 10899  
|||||  
DY 2047 tgcagtgagcagagatcacaccactgtcaccttagccttggtgtgacagagcaagactgtgtc 2106  
|||||  
DB 10899 TGCAAGGAGGCGAGATGATGTCACATCGCATGCTGAGCTTGACCAAGAGCAAGACTCTGTC 10958  
|||||  
DY 2107 taaaaaacaaaacaaaacaaaacaaaacaaaacaaaac 2141  
|||||  
DB 10959 TCAAAACAAAAGAAAGCAAACAAAACAAAACAAAGA 10993

RESULT 12  
C\_0207

ID 010207 standard; cDNA; 1618 BP.  
AC 010207;  
DJ 19-MAR-1991 (first entry)  
DE pMHC insert containing Human cytokine synthesis inhibitory  
DE factor  
KW Delayed-type hypersensitivity; DTH; leishmaniasis; parasite;  
KV MHC-associated autoimmune disease; Interferon-gamma; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT cds 33..566  
FT /tag= a +  
DR EP-405980-A.  
PN 02-JAN-1991.  
PD 28-JUN-1990; 307091.  
PT 28-JUN-1989; US-372667.  
PR 20 JBC-1989; US-453951.  
PA (SCHE ) SCHERING CORP.  
PI Kosman TR, Moore KW, Bond MW, Vieira PWM;  
DR 1; FJSD; R10158.  
PM mammalian cytokine synthesis inhibitory factors - capable of  
PC inhibiting synthesis of cytokines(s) associated with delayed-type  
PP hypersensitivity and useful in treatment of e.g. leishmaniasis  
PS Disclosure: Fig 4; jimp; English.  
CC The gene product may be used in treatment of diseases associated

CC With MHC-linked immune response, suppressing a cell mediated or  
CC humoral immune response. It may specifically be used to treat  
CC delayed-type hypersensitivity, leishmaniasis, and immune disorders.  
SQ Sequence 1618 BP; 461 A; 369 C; 356 G; 432 T;

Query Match 5.9%; Score 236.4; DB 1; Length 1618;  
Best Local Similarity 80.7%; Pred. No. 8e-49;  
Matches 276; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

OY 1790 ccatgtttgtgctatataaacctttaaagcttgcggtggtccggtgctacgcc 1849  
DB 1137 CCAGCTGTATTATTAACCACTTAATTTGGTTACAGCGCGCGCGGCTACGCC 1196  
OY 1850 tgaataccagcaatttgagagtcgagcgagcgagcactcagagtcagagttccag 1909  
DB 1197 TGTATCCAGCAGCTTTGGAGGCTGAGCGGCTGAGTCACTTGAGGTCAAGGATTCTA 1256  
OY 1910 accagcctgacccaatgtgtaaacctctctactactaaatacaaaataactgggt 1969  
DB 1257 ACCAGCTGTGTAACATGTTGTAACCCCGTCTACTATAAATAAATAATAGCGGGC 1316  
OY 1970 gtagtgagcggtgctgttaattccagactcagggagcgagcgaggtgatttga 2029  
DB 1317 ATGCTGGCGCGACCTGTATCCAGTACTTGGAGGCTGAGGCAAGAAATTCCTGA 1376  
OY 2030 acctggagagtgaggttgagcagagatcacacacactcagctcagcttggtga 2089  
DB 1377 ACCCAGAGATGGAAGTTGCACTGAGCTGATTCATGACCCCTTACTCCAGCTGGGTGA 1436  
OY 2090 cagagcaagactctgtctaaatacaaaacaaacaaacaa 2131  
DB 1437 CAGAGCAAGACTCTGTCTCAAAAAATAAATAAATAAATAA 1478

RESULT 13

ID Q46958 standard; CDNA; 1618 BP.

AC Q46958;

DE 25-JAN-1994 (first entry)

KW Human cytokine synthesis inhibitory factor clone pH15C.

KW Mammalian cytokine synthesis inhibitory factor; CSIF; Interleukin 10;

KW IL-10; immune system imbalance; human T cell; Leishmaniasis;

KW rheumatoid arthritis; systemic lupus erythematosus; thyroiditis;

KW myasthenia gravis; insulin-dependent diabetes mellitus; ss.

OS Homo sapiens.

FT Key location/Qualifiers

FT cds 31..567

FT mat\_peptide 85..564

FT /tag a

FT /tag b

FT /product mature\_CSIF

PN US5231012-A.

PD 27-JUL-1993

PF 28-JUN-1988; 372667.

PR 28-JUN-1988; US-372667.

PR 20-DEC-1989; US-453951.

PR 06-AUG-1990; US-546235.

PR 20-JUL-1992; US-917806.

PA (SCHE) SCHERING CORP.

PI Bond MW; Moore KW; Mosmann TR; Vieira PJM;

DR WPI; 93-249726/31.

DR P-PSDB; R39714.

PT Genes and proteins encoding cytokine synthesis inhibitory factors

PT - useful in treating diseases associated with cytokine

PT imbalances, e.g. parasitic infections and auto-immune disorders

PS Claim 1; Fig 4; 23pp; English.

CC A human T cell cDNA library was screened with probes based on the

CC murine CSIF gene. Two clones carrying plasmids pH5C and pH15C were

CC identified. (These two expression vectors are claimed). The CSIF

CC polypeptide they encode inhibits synthesis of cytokines associated

CC with delayed type hypersensitivity responses. CSIF (also called IL-

CC imbalances, such as leishmaniasis and MHC-associated autoimmune  
CC diseases caused by excessive production of interferon-gamma, e.g.  
CC rheumatoid arthritis, SLE, IDDM, myasthenia gravis and thyroiditis.  
SQ Sequence 1618 BP; 463 A; 367 C; 356 G; 432 T;

Query Match 5.9%; Score 236.4; DB 1; Length 1618;  
Best Local Similarity 80.7%; Pred. No. 8e-49;  
Matches 276; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

OY 1790 ccatgtttgtgctatataaacctttaaagcttgcggtggtccggtgctacgcc 1849  
DB 1137 CCAGCTGTATTATTAACCACTTAATTTGGTTACAGCGCGCGGCTACGCC 1196  
OY 1850 tgaataccagcaatttgagagtcgagcgagcgagcactcagagtcagagttccag 1909  
DB 1197 TGTATCCAGCAGCTTTGGAGGCTGAGCGGCTGAGTCACTTGAGGTCAAGGATTCTA 1256  
OY 1910 accagcctgacccaatgtgtaaacctctctactactaaatacaaaataactgggt 1969  
DB 1257 ACCAGCTGTGTAACATGTTGTAACCCCGTCTACTATAAATAAATAATAGCGGGC 1316  
OY 1970 gtagtgagcggtgctgttaattccagactcagggagcgagcgaggtgatttga 2029  
DB 1317 ATGCTGGCGCGACCTGTATCCAGTACTTGGAGGCTGAGGCAAGAAATTCCTGA 1376  
OY 2030 acctggagagtgaggttgagcagagatcacacacactcagctcagcttggtga 2089  
DB 1377 ACCCAGAGATGGAAGTTGCACTGAGCTGATTCATGACCCCTTACTCCAGCTGGGTGA 1436  
OY 2090 cagagcaagactctgtctaaatacaaaacaaacaaacaa 2131  
DB 1437 CAGAGCAAGACTCTGTCTCAAAAAATAAATAAATAAATAA 1478

RESULT 14

ID V35620/C standard; DNA; 32367 BP.

AC V35620;

DE 07-SEP-1998 (first entry)

KW Human SHOX (short stature homeobox containing gene) gene sequence.

KW Homeobox domain; human growth gene; growth regulation; growth defect;

KW Turner's syndrome; short stature homeobox containing gene; SHOXa;

KW SHOX; bone disease; osteoporosis; calcium regulation; short stature;

KW transcription factor A; ss.

OS Homo sapiens.

PI K09814568-AL.

PI 09-APR-1998.

PI 29-SEP-1997; E05355.

PI 16-JAN-1997; EP-100583.

PI 01-OCT-1996; US-027633.

PI (RAPP/) RAPPOLD-HOERBRAND G.

PI Rao E; Rapppold-hoerbrand G.

DR WPI; 98-271719/24.

PT New human growth genes - used to develop products for the diagnosis

PT and treatment of human growth defects such as short stature, e.g.

PT Turner's syndrome

FS Claim 19; Pages: 51-67; 84pp; English.

CC This is the human SHOX gene sequence containing the PAR1 region. The gene

CC region corresponding to short stature has been identified as a region of

CC approximately 500 kb in the PAR1 region of the X and Y chromosomes. Three

CC genes in this region have been identified as candidates for the short

CC SHOX93 or HOX93). pT92 and SHOT (SHOX-like homeobox gene on chromosome

CC three). The SHOX gene has two separate splicing sites resulting in two

CC variations: SHOXa and SHOXb. The specification provides sequences of SHOX

CC (short stature homeobox-containing) genes SHOX E792, SHOXa, SHOXb, SHOT

CC and exons of the SHOX genes as shown in V35610 to V35621 and protein

CC sequences of the human growth protein transcription factor SHOXa, SHOXb

CC and SHOT as shown W60573 to W60575. The novel genes are responsible for

CC human growth. Defects in the genes can cause short stature, e.g.

CC Turner's syndrome. The products can be used to develop agents for the

CC treatment of short stature or other human growth disorders. The products





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RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
23	449.2	11.2	454	51	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
24	448	11.2	448	42	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
25	448	11.2	448	48	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
26	448	11.2	448	63	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
27	447.2	11.2	452	63	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
28	447	11.1	447	44	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
29	447	11.1	448	44	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
30	444	11.1	444	45	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
31	444	11.1	444	47	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
32	443.4	11.1	445	41	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
33	443	11.1	443	49	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
34	443	11.1	444	63	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
35	442	11.0	444	28	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
36	437.6	10.9	444	62	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
37	435	10.9	435	43	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
38	432	10.8	433	36	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
39	431	10.8	431	34	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
40	430.2	10.7	436	41	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
41	429.4	10.7	434	40	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
42	424.4	10.6	440	31	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
43	424.4	10.6	437	42	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
44	424	10.6	424	61	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
45	420	10.5	420	45	AI088738	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x

## ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
2	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
3	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
4	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
5	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
6	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
7	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
8	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
9	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
10	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
11	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
12	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
13	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
14	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
15	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
16	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
17	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
18	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
19	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
20	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
21	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
22	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
23	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
24	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
25	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
26	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
27	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
28	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
29	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
30	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
31	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
32	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
33	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
34	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
35	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
36	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
37	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
38	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
39	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
40	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
41	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
42	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
43	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
44	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x
45	AI401218	673 bp	EST	30-MAR-1999	AI744242	tr08a05.x	AI088738	ga16f11.x	AI088738	ga16f11.x	AI088738	ga16f11.x

## BASIC COUNT

Query Match 15.6%; Score 627.4; DB 46; Length 673;  
 First local similarity 96.1%; Pred. No. 5.5e-107;  
 Matches 643; Conserved 0; Mismatches 26; Indels 0; Gaps 0;

AI401218 673 bp mRNA EST 30-MAR-1999  
 similar to SW:1131\_HUMAN P78552 INTERLEUKIN-13 RECEPTOR ALPHA-1  
 CHAIN PRECURSOR ; mRNA sequence.

AI401218 94244305  
 AI401218.1 GI:4244305  
 EST.

human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 673)  
 NCI/NIHSD-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index  
 Unpublished (1998)  
 On Apr 7, 1998 this sequence version replaced gi:3035192.

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 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldi, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html

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 Seq primer: -40UP from Gibco  
 High quality sequence stop: 450.  
 Location/Qualifiers  
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 /clone="IMAGE:2103714"  
 /clone\_lib="NCI CGAP Brn23"  
 /tissue\_type="glioblastoma (pooled)"

RESULT 2  
 LOCUS AI768613 624 bp mRNA EST 28-JUN-1999  
 DEFINITION WH24a04.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2381646 3'  
 similar to SW:1131\_HUMAN P78552 INTERLEUKIN-13 RECEPT

ACCESSION A1768613  
 NID 95235122  
 VERSION A1768613.1 GI:5235122  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 624)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL On Dec 20, 1995 this sequence version replaced gi:1134640.  
 COMMENT

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 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html

Seq primer: -40UP from Glibco  
 High quality sequence stop: 475.  
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1. 624  
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 /map="9"  
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 /lab\_host="DH10B"  
 /note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI-CGAP\_Kid3 was  
 prepared, and 8S circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (clonids 1322376-1323911, 1456007-1456755, and  
 1500552-1502855). Subtraction by Bento Soares and M.  
 Fatima Bonaldo.  
 BASE COUNT 176 a 123 c 115 g 208 t 2 others  
 ORIGIN

Query Match 15.28; Score 609.4; DB 59; Length 624;  
 Best Local Similarity 99.48; Pred. No. 1.2e-103;  
 Matches 621; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 Oy 784 cagaatttttagcagatgcctattatgaagtagaagtcataacagcaacagcgag 843  
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 Db 624 CAGAAATTATAGCAATGCTTTATGAGACTAGAAGCAATTAACGCCAATCTGAG 565  
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 Oy 844 acacataagttttctacgtccagagggcctaattgagaatccagaatttgagaagaat 903  
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 Db 564 ACACATATATTTTCTACGACGCAAGAGCTTAATAGTAAGATCCAGATTTGAGAGAAT 505  
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 Oy 904 gtggagaatcatctgtttcatcgtccctgggtgttcttcgttactttgaacagtc 963  
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 Db 504 GTGGAGATATCATCTTTTCATGCTCCCTGGTGTCTTCTCTGATCTTGAACACAGTC 445  
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 Oy 964 agataagagtcacaaacaaatagtaagtcatagagtagcaaacctcgagtaattgg 1023  
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 Db 444 AGATAAGAGTCACAAACAAATTAATTAATGATAGAGATGACAAACTCTGAGAGTAATGG 385  
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 Oy 1024 agccaaagaatgagtagtaagtagcgaattccacactctacataacacattactc 1083  
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1b 384 AGCCATGAAATGATATAGGTAAAGACGCAATTCACACTCTACATTAACCATGTTACTC 325  
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 Oy 1084 atttttcagtcacgtcgcgagtagtcataatagttactcgtcttaacctaagaagctc 1143  
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 Db 324 ATTCTTCAGTACATCGTCGCGAGGTGCAATCATACTCTCTGCTTTACTT-AAAAGCTC 266  
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 Oy 1144 agattatattatccctcccaatctcgtatccctgagcaagaattttaagaagtgttga 1203  
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 Db 265 AAGATTATTATATTCCTCCCAATTCCTGATCCCTGGCAAGATTTTAAGAATGTTTGA 206  
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 Oy 1204 gaccagaatgactactctgactgactgagaagtagacatctatgagaagcaacaag 1263  
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 Db 205 GACCGAATATGATGATCTGCACTGCAAGAGATGACATCTATGAGAACCAACCAAG 146  
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 Oy 1264 gaggaaacgactctgagtgctgatatagaacacgtgagaagaagcctcagtagtga 1323  
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 Db 145 GAGGATACCGACTGTGTAGTGTGATGAAACCTGAGAAAGCCTCTCAGTATGAGA 86  
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 Oy 1324 taattatttttactcactgactgactgagaagattcttccatctccattgtat 1383  
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 Db 85 TAATTATTTTACTGCTGACTGACTGGAAGATTCCTCCATTCCTCATTTGTAT 26  
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 Oy 1364 ctgggaacttataatgagaactg 1408  
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 Db 25 CTGGGAACCTATTATTAATGAAACTG 1  
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REVISED 3  
 AA523414/c 596 bp mRNA EST 21-AUG-1997  
 LOCUS ng30a07.s1 NCI-CGAP\_C03 Homo sapiens CDNA clone IMAGE:936276 3'  
 DEFINITION mRNA sequence.  
 ACCESSION AA523414  
 NID 92264126  
 VERSION AA523414.1 GI:2264126  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 596)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL On May 18, 1995 this sequence version replaced gi:810992.  
 COMMENT

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 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,  
 M.F., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arraying: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html

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 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 472.  
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 /clone="IMAGE:936276"  
 /clone\_lib="NCI-CGAP\_C03"  
 /sex="pooled"  
 /tissue\_type="colon"  
 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from 12 pooled bulk tumor samples and primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization.

BASE COUNT 207 a 135 c 103 g 151 t  
ORIGIN

Query Match 14.8%; Score 592.8; DB 34; Length 596;  
Best Local Similarity 99.7%; Pred. No. 1.5e-100;  
Matches 594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3401 agaatattgtttctctgataagaaatgaatattcttccagatattatattat 3460  
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Db 596 AGAATATTGTTTCTCTGATGAGATGATTAATCTTCCAGATATTATATT 537  
QY 3461 ctgggaagcaaaaccatgcctccctcagcattttactgtatctattagatgc 3520  
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Db 536 CTGGGAAGCAAAACCCATGCCCTCCCTAGCCATTATTACGTTATCTTATTGATGCG 477  
QY 3521 catgaagaagatgtgtgaaattcccaaaacttatgtctgacatctatgcagcttg 3580  
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Db 476 CATGAAGAGATGCTGTGAATTCACAACAACATTGATGCTGACATGACGCTGG 417  
QY 3581 gaatgggaagtgatctcttcttccatctctctcttcttcttcttcttcttcttctt 3640  
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Db 416 GAGTGGGGAAGTATCTTTGTTCCATCTCTCTTTAGCAATAAATAGCTGAGGGA 357  
QY 3641 aaagggaggaagaaagaaatgataggaatcctgtgtgtgtgtgtgtgtgtgtgtgt 3700  
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Db 356 AAAGGGGAGGAAAGGAAGTATGGAATACCTGTGTGTGTGTGTGTGTGTGTGTGTGTG 297  
QY 3701 gaagctctgagtggt 3760  
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Db 296 GAGCTCTTGAGGT 237  
QY 3761 catttactgtttttagtgctatgctatgttgatatttcttcttcttcttcttcttcttctt 3820  
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Db 236 CATTACTGTTTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 177  
QY 3821 gtttcagagatgtgaattcttcttcttcttcttcttcttcttcttcttcttcttctt 3880  
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Db 176 GTGTGAGAGATGATTAATCTTATCTTCTGTTCACTTAACTTTTCCCTATCTGAGGAC 117  
QY 3881 tgaaggagatgtgaagaatgttaacattttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3940  
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Db 116 TGAAGGATATGTGAACAATGTTACATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 57  
QY 3941 gtttaactcttataagaaagcttgataataataatctgtcttcttcttcttcttcttctt 3996  
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Db 56 GTTAACTTCTTATAGGAAGCTTGAATAAATAATATGTTCTTTTGTATGTCA 1

RESULT 4  
AI888989/c 627 bp mRNA EST 01-SEP-1999  
LOCUS A1888989 x1 NCI CGAP Kid2 Homo sapiens cDNA clone IMAGE:2402953 3'  
DEFINITION similar to SW:1131\_HUMAN P78552 INTERLEUKIN-13 RECEPTOR ALPHA-1  
CHAIN PRECURSOR ; mRNA sequence.

ACCESSION A1888989  
NID 95594153  
VERSION A1888989.1 GI:5594153  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 627)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT On Jun 5, 1998 this sequence version replaced g1:3188446.

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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbp/image/image.html

Seq primer: -400P from Glibco  
High quality sequence stop: 388.

F3A7JRES  
source

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/db\_xref="taxon:9606"  
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/note="Organ: kidney; Vector: pTZ19-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Plasmid DNA from the normalized library NCI-CCGAP Kid2 was  
prepared, and ss circles were made in vitro. Following HAP  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(clones 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 172 a 137 c 108 g 210 t  
ORIGIN

Query Match 14.7%; Score 590.8; DB 62; Length 627;  
Best Local Similarity 98.6%; Pred. No. 3.4e-100;  
Matches 617; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Db 627 AAAAGCTCAAGATTAATTAATTCCTCCATTCCTGATCTCGGCAAGATTTTAAAGAA 568  
QY 1195 atgtttggagaccagaatgatactctgtcactgtgaagaagtaacatctatagaag 1254  
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Db 567 ATGTTTGGAGACCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 508  
QY 1255 caaaccaaggagaaacgactctgtgactgataagaacctgaagaacccctctg 1314  
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Db 507 CAACCAAGAGGAACCAACCACTGTGATGCTGATGATGATGATGATGATGATGATGATG 448  
QY 1315 tgaaggagataatttttaccctcactgtgaccttgaagaagattcttccattctcc 1374  
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Db 447 TGATGAGATTAATTTATTTTACCTTCACTGAGACTTGAAGATCTTCCATTCTCC 388  
QY 1375 attgttactcgggaacttattaaatgaagaactgaactcgtcaccatttaaaacagg 1434  
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Db 387 ATTTGTTATCTGGAGACTTAATTAATGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 328  
QY 1435 cagctcataagagcccaagcttcttatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1494  
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Db 327 CAGCTCATAGAGCCACAGCTTTATGTTGATGCTGCGCACGAAAAAATAAATAAATAG 268  
QY 1495 ggcgctttggagaggtgttgagtcattctcattgaattataaagcagcagcttca 1554  
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Db 267 GCGGCTTTGGAGAGAGTGTGAGTATCTCATTTGAATTAATAAAGCAAGCAAGCTTCA 208  
QY 1555 aactaaggagacaaagcaaaatgatgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1614  
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Db	207	AACTAGGGGACACAACACAAAAGTGAATGATGTAGTGAGACTTAATCTTATCAAGAAGTTGTG	148
Oy	1615	aaactctctgtggggaatcatacttcgtcttggttctttgtgtcaacatgacaacaatttt	1674
Db	147	ACAACTTCTCGTAGGGGATCATTAATTGCTTCCTTGTTCTTGTCACAAATGAACAAATTTTT	88
Oy	1675	atttgtaggggagaccatctt- <u>g</u> gggtgcacaatgct-aatgtcaaaccttgatgcacaaga	1732
Db	87	ATTGTTAGGGGACACTCATTTCGGGGGTGCACAAATGCTAATATGTCAAACTTGATGTCACAAAG	28
Oy	1733	acatgtagaaaaacaaaattgatataaa	1758
Db	27	ACATCTAGGAACAAACAAATGAGATAA	2
RESULT	5		
LOCUS	AL036221		
DEFINITION	AL036221	673 bp	mRNA
KEYWORDS	DKRZP5641I202.r1.564 (synonym: hfbp2)	Homo sapiens	cDNA clone
ACCSSION	AL036221		
NID	93405818		
VERSION	AL036221.1	GI:5405818	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 673)		
	Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and		
	Miemann,S.		
	EST (Duesterhoeft, et al.)		
JOURNAL	Unpublished (1999)		
COMMENT	On Jun 22, 1998 this sequence version replaced gi:3246899.		

**CONTACT:** Duesterhoeft A  
 MIPS  
 Am Klopferstutz 18a D-82152 Martinsried, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by Qiagen within the cDNA sequencing consortium of the  
 German Genome Project.  
 No sl sequence available.  
 This clone is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
**LOCATION/QUALIFIERS**  
 1. .673

	Query Match	14.3%: Score 574.8; DB 61; Length 673;
	Best Local Similarity	96.6%: Pred. No. 3.2e-97;
	Matches 650; Conservative	0; Mismatches 15; Indels 8; Gaps
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Db	2 GGGGGGGGGGGGGCCGCCGCTACGGAACACTGACCACCTGATGACAAATTGAGTG	61
Qy	152 tctctgttggaacctctgcacagcgaatctatgtgacatggaatccaccgccggggagccagct	211
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Oy	212	caattttagctctgtgattttagtcaattttagcgcaacaagaatgaagaattagctc	271
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Dd	122	CAATTGTAAGCTATAGGATTTATTGATCTTTTGGCACAACAAGATAGAAAATAGCTC	181
Oy	272	cggaaactcgtctgtcaatagaagatccctcgataatgagaagatttgcctgcgaagtgggt	331
Dd	182	CGGAAGATCGTGCTTCAATAGAGTAGACCCCTGATGAGAGGATTTGTCTGCAAGTGGGT	241
Oy	332	ccccggttagcaccaatgagagtgagagaagcctctgcaatttggttgaaaaatgcattctac	391
Lj	242	CCCGATGTAGACCAACAAGAGAGTAGAGAGAGCTGACATTTTGGTGAATAATCATCTCAC	301
Oy	392	ccccgaagtgatgcctgcagtcgtcgtgtagctagcttaatgcaatttggcaaacctga	451
Dd	302	CCCCAGAGGAGTAGTCCATGAGTCTGCTGTAGCTAGCTTCAATGACTTTTGGCACAACCTGA	361
Oy	452	gctacatgaagtgtctcttgctccct-ggaaggaatacagctccgcgaactatact	510
Lo	352	GCTCATGAGAGTGTCTTGCTCCCTGGGAGGAGATACAGTCCGACACTATAGTACT	421
Oy	511	ctctactattggcagagaagcctggaaaaaatcatcaatgtgaaaaacatcttagaga	570
Dd	422	CTTACTATTGGCACAAGACCTGGAAGAAA-TCATCAATATGGAAGAACTCTTTANAGAA	480
Oy	571	ggcgaacttggtttctctttagcttgcacccaagaatgaagattcagtttitaaga	630
Dd	481	GGCCAAATACCTTGGTGTATCTCTTGTGATCGACCAAAAGTAAAGGATTCAGATTTPAACA	540
Oy	631	cacagtg-tocaataatgtcaagaatataatcaggaanaatlaaacatccttcaat-	688
Dd	541	CACAGTGGTCCAAATATAGTGTCAAGGATATGACAGAAATAATTAACCATCTTCANNT	600
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Oy	746	tucacaatgata 758	
Dd	667	TCGACAGTGATGA 673	

RESULT 6  
 A1816791/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 NIT  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

A1816791 571 bp mRNA EST 24- AUG-1999  
 WJ34509.x1 NCI-CGAP\_kid2 Homo sapiens cDNA clone IMAGE:240469 3  
 similar to SW:1131\_HUMAN P7852 INTERLEUKIN-13 RECEPTOR ALPHA-1  
 CHAIN PRECURSOR ; mRNA sequence.  
 A1816791  
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 A1816791.1 GI:5435870  
 EST.  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Euarcharya; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 571)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute. Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 On Jul 5, 1998 this sequence version replaced gi:3186971.

Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert\_Strausberg@nih.gov  
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMNI at:  
[www-dio.llnl.gov/dbvp/image/image.html](http://www-dio.llnl.gov/dbvp/image/image.html)





Db	Accession	LOCUS	DEFINITION	ORGANISM	KEYWORDS	REFERENCE	TITLE	JOURNAL	COMMENT
Db	246	ACATCTTTAGAAACGCCAATACCTTGGTTGGTTCTTTGATCTGACCAAGTGAAGGAT							
Qy	617	ccagtttgcgaacacacacagttgccaaataatggtcaagataatgacggaataaac							
Db	306	CCAGTTTGGAAACAAACACAGTGTCCAAATAATGGTCAAGATTAATCAGAGAAATTAAC							
Qy	677	catcttcaataatagtgcttcaattacccggtgataaacctgatactccacatat							
Db	366	CATCCTTAATAATATATGCTTTAACTTCCCGTGTAAACCTGATCCTCCACATATTA							
Qy	737	acctctccctccacacatgatgacctataatggtcaatggagataccacagaatt							
Db	426	ACCTCTCCTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAGATTT							
Qy	797	gcagatgacctatttatgaaagtagaagtcataacacagccaacatcgaga							
Db	486	GCAGATGCCCTATTTATGTAAGTAAGTCAATTAACAGCCAACTGAGA							
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DEFINITION		mrna sequence.							
ACCESSION		AI887705							
NID		g5592869							
VERSION		AI887705.1	GI:5592869						
KEYWORDS		EST.							
SOURCE		human.							
ORGANISM		Homo sapiens							
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;							
		Eutheria; Primates; Catarrhini; Homiidae; Homo.							
		1 (bases 1 to 521)							
		NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .							
		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),							
		Tumor Gene Index							
		Unpublished (1997)							
		On Jun 5, 1998 this sequence version replaced gi:3187155.							

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: [Robert.Strausberg@nih.gov](mailto:Robert.Strausberg@nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www-bio.llnl.gov/dbfp/Image/Image.html](http://www-bio.llnl.gov/dbfp/Image/Image.html)

## FEATURES

### source

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primer: -40UP from GlbCo
n quality sequence stop: 408.
Location/Qualifiers
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/db_xref="taxon:9606"
/map="21q.56cM"
/clone="IMAGE:2436213"
/clone_1bp="NCI CGAP UC4"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: oligo dr
Average insert size 1.48 kb. Life Technologies catalog #
11542-016"

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BASE COUNT	179 a	121 c	92 g	129 t
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	Matches 521	Conservative 0	Mismatches 0	Indels 0
CY	3476	caagctccccctagaccatttttactgltatccctatttagacacccatgaaagatgct	3535	
Db	521	CATGCTCCCTCCCTACCCACATTTTACTGTATTCCTATTAGAGGCCATGAAGAAGATGCT	462	
CY	3536	gtgaattccccacaacaacatgatgctgcagtcacgtcagctcgtggagtgaggaaatgat	3595	
D	461	GTGAATTCGCCAACAAACATTGATCTGACATCATATGCAAGCTTGGGAGTGGGAAATGAT	402	
CY	3596	ctttgttcccactcctctctcttttagcagtaaaatagctgaggagaaaggaggagaaag	3655	
Db	401	CTTTGTTCCTCCATCCTCTCTTTTAGCATAAATTAAGCTGACGAGGAAAGAGGAGGAAAG	342	
CY	3656	gaagattagggaaatccctgtagtggtttttagatcccttagctcttggagagctcttgaaggtg	3715	
Db	341	GAAAGTATGGGAATACCTGTGGTGTGTGATCCCTAGCTCTTGGAGCTCTTGGAGGTG	282	
CY	3716	tctgatacagtgatattcccaaccctcgttgggaaattagtaagctcatctagttttag	3775	
Db	281	TCTGATCAGTGTGATTTCCATCCCTGTGGGAATTAATAGTGCATTTACTGTTTAG	222	
CY	3776	gtctagcctatgtgtaatttttctctaaacatacctaagcaaacccagtgctcagatggtca	3835	
Db	221	GCTATGCCATATGTGATTTTTCCTAACATACCTTAAGCAAAACCCAGTGCAGAGATGTAA	162	
CY	3836	tctctatctcttcgttcagtaagtttctccctcatctcgggcactcgaaggagatatgta	3895	
Db	161	TTCTATTTCCTTCGTTCACTTAAGTTTTCCTTATCTGGGCACTGAAGGATATGTCA	102	
CY	3896	aacaaatjtaaacatttttggtagtctccaacacaggaatgtttctgtttbaactctctata	3955	
Db	101	AACAAATGTAAATTTTGGTAGTCTTCAACACAGGATGTTCCTGTTAACTTTTATA	42	
CY	3956	ggaagcttgagtaaaataaataatgctctttttagatgca	3996	
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DEFINITION	AA669035	507 bp	mRNA	EST
ACCESSION	ab886g12.5	Stratagene	lung (#337210)	Homo sapiens
NID	IMAGE:854085	3'	cDNA	clone
VERSION	AA669035			
KEYWORDS	52630534			
SOURCE	AA669035.1	GI:2630534		
ORGANISM	human			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1. (bases 1 to 507)			
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, K.,			
	Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,			
	Martin, J., Moore, B., Scheinberg, K., Stepec, M., Tan, F.,			
	Thaising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.			
TITLE	Unpublished (1997)			
COMMENT	On Nov 6, 1997 this sequence version replaced gi:332221.			

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: [est@wustl.edu](mailto:est@wustl.edu)  
 This clone is available royalty-free through LINT; contact the  
 IMAGE Consortium ([info@image.lnll.gov](mailto:info@image.lnll.gov)) for further information.  
 Seq primer: -40ml3 fwd. 5' from Amerham  
 High quality sequence stop: 455.  
 Location/Qualifiers











GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

Run on: January 19, 2000, 17:31:45 ; Search time 34.07 Seconds  
(without alignments)  
264.183 Million cell updates/sec

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Scoring table: BLOSUM62
Searched: 188963 seqs, 23686106 residues
Database : A.Geneseq_36:*
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Number of hits that pass the threshold : 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2104	100.0	380	1	W35295	Human IL-13 bindin
2	2104	100.0	380	1	W36513	Human zcyto2 cyto
3	2104	100.0	380	1	W41502	Human cytokine/pep
4	2104	100.0	390	1	W33603	Hom sapiens HR-1
5	2104	100.0	380	1	W24972	Human interleukin-1
6	2104	100.0	380	1	W41520	Human HR-1 recepto
7	2078	98.8	380	1	W36510	Human zcyto2 cyto
8	1853	88.1	372	1	W36616	Cebus macaque zc
9	1753	83.3	359	1	W56260	Construct containi
10	1753	83.3	315	1	W56261	Mature interleukin
11	1194	56.8	383	1	W35294	Murine IL-13 bindi
12	456	21.7	157	1	W56252	Interleukin-13 bin
13	311.5	14.8	396	1	R23216	Sequence of human
14	311.5	14.8	420	1	R23219	Sequence of secret
15	311.5	14.8	396	1	R23220	Sequence of secret
16	311.5	14.8	420	1	W82842	Human interleukin-
17	310.5	14.8	420	1	R25064	Human IL-5 recepto
18	305.5	14.5	420	1	R22215	Sequence of human
19	287	14.1	313	1	W21856	Protein used in pr
20	256	14.1	426	1	W09891	Mouse interleukin-
21	295.5	14.0	427	1	W24973	Human interleukin-
22	294.5	14.0	426	1	W09892	Human interleukin-
23	292.5	13.9	1026	1	R70121	IL5-R-GPB 130 fusi
24	292	13.9	335	1	R25063	Soluble human IL-5
25	292	13.9	335	1	R33699	shIL-5R-alpha, Deo
26	249.5	11.9	155	1	W56255	Interleukin-13 bin
27	248	11.8	398	1	R22212	Sequence of interl
28	247	11.7	415	1	R22211	Sequence of interl
29	247	11.7	415	1	R22217	Sequence of interl
30	229	10.9	332	1	R22213	Sequence of interl
31	229	10.9	315	1	R22214	Sequence of interl
32	229	10.9	332	1	R23218	Sequence of interl
33	230	10.5	369	1	R47148	IL-2 receptor gamm
34	219	10.4	347	1	R47149	IL-2 receptor gamm
35	209.5	10.0	369	1	R55094	Murine IL-2R gamma
36	209	9.9	482	1	W31646	Human cytokine rec
37	207	9.8	252	1	R47150	IL-2 receptor gamm
38	206	9.8	230	1	R47151	IL-2 receptor gamm
39	201.5	9.6	230	1	R82934	Interleukin 4 comp

40	195	9.3	878	1	R78608	Mu1ine IL-3 recept
41	194	8.2	878	1	R93529	Fas sequence from
42	185.5	8.8	154	1	M56257	Interleukin-13 bin
43	180.5	8.6	637	1	R20932	Sequence of Beta-C
44	179	8.5	600	1	R78610	Expression vector
45	179	8.5	596	1	R78616	Expression vector

## ALIGNMENTS

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3W55295 startCard; Protein; 380 AA.
4W55295;
527-MAR-1996. (first entry)
6Human IL-13 binding chain of the IL-13 receptor.
7Interleukin-13. IL-13; interleukin-13 receptor binding chain; IL-13pc;
8mediator; IL-13 receptor binding inhibition; Ige-mediated condition;
9allergy; asthma; immune complex disorder.
10Homo sapiens.
11Key
12Peptide
13Location/Qualifiers
141..25
15/label= signal_sequence
16/note= "putative"
1726..380
18/label= mature_protein
1926..341
20/label= extracellular_domain
21342..362
22/label= transmembrane_domain
23363..380
24/label= intracellular_domain

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MO99731346-AL  
04-SEP-1997  
28-FEB-1997. 003124  
01-MAR-1996: US-609572.  
(GEMV) GENETICS-INST-INC.  
Collins M, Donaldson D, Filtz L, Neben T, Whitters M,  
Wood C;  
WIT: 97-448632/41.  
V-SDS: T95214.  
New nucleic acid encoding interleukin-13 receptor binding chain and  
transformed cells - proteins, antibodies and inhibitors, for  
treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
and in diagnosis  
Claim 11, Pages 34-35; 49pp; English.  
The present sequence represents the human interleukin-13 (IL-13) binding  
chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a  
mediator of the known biological activities of IL-13. Recombinant  
IL-13bc proteins, and antibodies raised against them, are used to  
inhibit the binding of IL-13 to its receptor. They are particularly used  
to treat IGE-mediated conditions, e.g. allergy, asthma and immune complex  
disorders, especially lupus, nephritis, thyroiditis and Grave's disease.  
They are also used to treat immune deficiency (particularly in  
haematopoietic progenitor cells), cancer etc., and to increase macrophage  
activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  
with such activity is combined with IL-13bc and the mixture applied,  
in vivo, to a cell expressing at least one chain of the IL-13 receptor  
other than IL-13bc. IL-13bc can also be used in diagnosis to detect  
expression of IL-13, its receptor or binding chain, and to raise specific  
antibodies which may be useful for treating some tumours.  
Sequence 310 AA:

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Query Match      100.0%; Score 2104; DB 1; Length 380;
367 Local Similarity 100.0%; Pred. No. 8.1e-194;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY . 1 MAFWCLYICLYTPIIISTTFCCSSSDPEIKVNPQDFEIDPGLGLGLYLQNPPLSLD 60  
1 MAWCLYICLYTPIIISTTFCCSSSDPEIKVNPQDFEIDPGLGLGLYLQNPPLSLD 60  
1 MAWCLYICLYTPIIISTTFCCSSSDPEIKVNPQDFEIDPGLGLGLYLQNPPLSLD 60



QY 61 HEKECEVEYELKRNIGSEWTKIITRNHLHYKGFPLNKGIEAKIHITLLPMQCTNSEVQ 120  
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 DB 121 SSWAETTYWISPGIPEETKVQDMCYVNMQYLLCSMKRPGIGVLLDTNLYFWYEGLDH 180  
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 DB 181 ALQCVYIRKADGONICRPFYLEASDYKDFYICVNSSSEKPIRSSYFTFOLQNIYKPLP 240  
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 DB 241 PYVLTFTRESSCEIKLWMSIPLGPIPARCFDYIEIREDDTLVTATVENEYTLTKTNE 300  
 QY 301 TROLCFVRSKVNIVYCSDDGIMSEWSDKQCEGEDLSKRTLLRFWLPFGFILLVIFVTG 360  
 DB 301 TROLCFVRSKVNIVYCSDDGIMSEWSDKQCEGEDLSKRTLLRFWLPFGFILLVIFVTG 360  
 QY 361 LLRKPNTPPKMIPEFCDT 380  
 DB 361 LLRKPNTPPKMIPEFCDT 380

RESULT 2  
 ID W36613 standard; Protein: 380 AA.  
 AC W36613;  
 DE Human Zcytor2 cytokine receptor protein.  
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 OS Homo sapiens.  
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 FT Domain /label= transmembrane\_domain  
 FT Domain 364..380  
 FT Domain /label= intracellular\_domain  
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 FT Domain /label= ligand\_binding\_domain  
 PN W09733913-A1.  
 PD 18-SEP-1997.  
 PE 12-MAR-1997; US-013345.  
 PR 13-MAR-1996; US-013345.  
 PA (ZYMO) ZYMOGENETICS INC.  
 PI Baumgartner JW, Parrish TM, Foster DC, Grant FU,  
 PI Ohara FJ;  
 DR MPI: 97-470820/43.  
 DR N-PSDB: T96782.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Claim 2; Page 47-48; 79pp; English.  
 CC This sequence represents a novel ligand-binding receptor, Zcytor2,  
 CC which shares homology with cytokine receptors and was isolated from human  
 CC placental polyA+ RNA. The resulting polypeptide is a receptor for  
 CC cytokines (particularly interleukin-13) and is expressed on the surface  
 CC of testicular cells, probably being involved in spermatogenesis. It can  
 CC be used to detect ligands that promote proliferation and/or  
 CC differentiation of such cells in cultures and may also be used to treat  
 CC infertility. Antagonists of this receptor may be used to characterise  
 CC ligand-receptor interactions and as male-specific contraceptives. By  
 CC blocking the action of IL-13, receptor antagonists and ligand-binding  
 CC this receptor can also be used to modulate immune function, e.g. in  
 CC allergy and asthma, as a diagnostic to determine circulating levels of  
 CC ligand and also to isolate and purify ligands. Antibodies can be used to  
 CC assay circulating receptor (an abnormal level may be indicative of  
 CC disease such as cancer), for labelling cells that express the receptor,  
 CC and therapeutically as antagonist.  
 CC Sequence 380 AA.

Query Match 100.0%; Score 2104; DB 1; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-194;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MAVVCAIAGLTYFLISTFGCTSSSDTEKVNPPDDFELYVDGTYGLYLLQWQPLSLD 60  
 QY 61 HEKECEVEYELKRNIGSEWTKIITRNHLHYKGFPLNKGIEAKIHITLLPMQCTNSEVQ 120  
 DB 61 HEKECEVEYELKRNIGSEWTKIITRNHLHYKGFPLNKGIEAKIHITLLPMQCTNSEVQ 120  
 QY 121 SSWAETTYWISPGIPEETKVQDMCYVNMQYLLCSMKRPGIGVLLDTNLYFWYEGLDH 180  
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 DB 181 ALQCVYIRKADGONICRPFYLEASDYKDFYICVNSSSEKPIRSSYFTFOLQNIYKPLP 240  
 QY 241 PYVLTFTRESSCEIKLWMSIPLGPIPARCFDYIEIREDDTLVTATVENEYTLTKTNE 300  
 DB 241 PYVLTFTRESSCEIKLWMSIPLGPIPARCFDYIEIREDDTLVTATVENEYTLTKTNE 300  
 QY 301 TROLCFVRSKVNIVYCSDDGIMSEWSDKQCEGEDLSKRTLLRFWLPFGFILLVIFVTG 360  
 DB 301 TROLCFVRSKVNIVYCSDDGIMSEWSDKQCEGEDLSKRTLLRFWLPFGFILLVIFVTG 360  
 QY 361 LLRKPNTPPKMIPEFCDT 380  
 DB 361 LLRKPNTPPKMIPEFCDT 380

RESULT 3  
 ID W41502 standard; Protein: 380 AA.  
 AC W41502;  
 DE Human cytokine/peptide receptor, HR-1 receptor.  
 KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;  
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /label= Sig\_peptide  
 FT Protein /label= Mat\_protein  
 FT Protein /note= "Claim 14"  
 PN EP-812913-A2.  
 PD 17-DEC-1997.  
 PE 04-JUN-1997; 303815.  
 PR 12-JUN-1996; US-017343.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMR) SMITHKLINE BEECHAM CORP.  
 PI Appelbaum ER, Hu J;  
 PI MPI: 98-034974/04.  
 DR N-PSDB: V04075.  
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to  
 PT increase resistance to infections in individuals with trauma and/or  
 PT burns  
 PS Claim 13; Page 27-28; 34pp; English.  
 CC This protein comprises a novel human cytokine/peptide hormone  
 CC receptor, designated HR-1 receptor. The amino acid sequence  
 CC was deduced from a cDNA clone (see V04075) isolated from a human  
 CC testis cDNA library. It shows 27% amino acid identity and 52%  
 CC similarity with the human interleukin-5 receptor. Also claimed are  
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an  
 CC agonist to the polypeptide, antibody against the polypeptide, an  
 CC antagonist that inhibits the activity of the polypeptide, a process  
 CC for diagnosing a disease, or a susceptibility to disease, related  
 CC to expression of HR-1 receptor, and a method for identifying  
 CC compounds that activate or inhibit the HR-1 receptor. HR-1



receptor protein and polynucleotides can be used for research, biological, diagnosis and (gene) therapy applications, e.g. to increase resistance to infections in individuals with trauma and/or burns, and to prevent, ameliorate, treat, diagnose and/or determine predisposition to asthma, allergic disorders or disorders of haematopoiesis induced by AIDS, aplastic anaemia, congenital or cyclic neutropenia or as a consequence of cytotoxic therapy of cancer, lymphoma, leukaemia and/or bone marrow transplantation.

Sequence 380 AA:

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8.1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGCLYTLFTSTFCTSSDTEIKVNPPOPEIYDPLGYLYLQWQPPSLD 60  
DB 1 MAFVCLAIIGCLYTLFTSTFCTSSDTEIKVNPPOPEIYDPLGYLYLQWQPPSLD 60  
QY 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNGKIEAKIHLLPQCNGSEVQ 120  
DB 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNGKIEAKIHLLPQCNGSEVQ 120  
QY 121 SSMAETTWISPGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDTNVLFWYEGLDH 180  
DB 121 SSMAETTWISPGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDTNVLFWYEGLDH 180  
QY 181 ALQCVDIKADGQNGRFPLEASDYKDFICVNGSSENNPINSYFTFLOINIVKPLP 240  
DB 181 ALQCVDIKADGQNGRFPLEASDYKDFICVNGSSENNPINSYFTFLOINIVKPLP 240  
QY 241 PVLITFTRESSCEIKLWMSIPLGPIPARCFYEIEIRDDTLTATAVENETYLKTTNE 300  
DB 241 PVLITFTRESSCEIKLWMSIPLGPIPARCFYEIEIRDDTLTATAVENETYLKTTNE 300  
QY 301 TROLCEVVRKVNICYSDDGIMSEMSDKQWEGEDLSKTLRLFWLPFGFILLIVIFVTG 360  
DB 301 TROLCEVVRKVNICYSDDGIMSEMSDKQWEGEDLSKTLRLFWLPFGFILLIVIFVTG 360  
QY 361 LLRKPNTPPKMIPEFCDT 380  
DB 361 LLRKPNTPPKMIPEFCDT 380

#### RESULT 4

ID W33603 standard; Protein; 380 AA.

AC W33603;  
DT 08-JUN-1998 (first entry)  
DE Homo sapiens HR-1 receptor.  
KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;  
KW syndrome; aplastic anaemia; neutropenia; cancer treatment;  
KW infection resistance; diagnosis; tumours; HR-1 receptor;  
KW asthma; allergic; haematopoietic disorder.  
OS Homo sapiens.  
FH key location/Qualifiers  
FT Peptide 1. 21  
FT /note- "signal peptide"  
PN W09747742-A1.  
PD 18-DEC-1997.  
PT 09-JUL-1996; U11459.  
PR 12-JUN-1996; WO-010262.  
PR 12-JUN-1996; US-017843.  
PA (HUMA-) HUMAN GENE SCI INC.  
PA (SMK-) SMITHKLINE BEECHAM CORP.  
PI Appelbaum ER, Hu J.  
PI MPI: 98-052309/05.  
DR N-PSDB: V02295.  
PT DNA encoding human cytokine-peptide hormone receptor - useful for  
PT treating preventing or diagnosing, e.g. lowered resistance to  
PT infection, asthma, allergy, or haematopoietic disease  
PS Claim 15; Fig 1; 75pp; English.  
CC The sequence is that of the human cytokine/peptide hormone receptor

(HR-1 receptor). This, or its activators or agonists, can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haematopoietic disorders, e.g. where induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia, neutropenia or cytotoxic treatments for cancer. Antagonists of the receptor, e.g. antibodies or fragments of it may be used to treat conditions associated with overexpression of the HR-1 receptor, e.g. those listed above. Antibodies may also be used to assay levels of HR-1 receptor overexpression of which may be diagnostic of tumours, by usual immunassays; to isolate and identify HR-1 receptor-expressing cells; or for affinity purification of the HR-1 receptor.

Sequence 380 AA:

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8.1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGCLYTLFTSTFCTSSDTEIKVNPPOPEIYDPLGYLYLQWQPPSLD 60  
DB 1 MAFVCLAIIGCLYTLFTSTFCTSSDTEIKVNPPOPEIYDPLGYLYLQWQPPSLD 60  
QY 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNGKIEAKIHLLPQCNGSEVQ 120  
DB 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNGKIEAKIHLLPQCNGSEVQ 120  
QY 121 SSMAETTWISPGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDTNVLFWYEGLDH 180  
DB 121 SSMAETTWISPGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDTNVLFWYEGLDH 180  
QY 181 ALQCVDIKADGQNGRFPLEASDYKDFICVNGSSENNPINSYFTFLOINIVKPLP 240  
DB 181 ALQCVDIKADGQNGRFPLEASDYKDFICVNGSSENNPINSYFTFLOINIVKPLP 240  
QY 241 PVLITFTRESSCEIKLWMSIPLGPIPARCFYEIEIRDDTLTATAVENETYLKTTNE 300  
DB 241 PVLITFTRESSCEIKLWMSIPLGPIPARCFYEIEIRDDTLTATAVENETYLKTTNE 300  
QY 301 TROLCEVVRKVNICYSDDGIMSEMSDKQWEGEDLSKTLRLFWLPFGFILLIVIFVTG 360  
DB 301 TROLCEVVRKVNICYSDDGIMSEMSDKQWEGEDLSKTLRLFWLPFGFILLIVIFVTG 360  
QY 361 LLRKPNTPPKMIPEFCDT 380  
DB 361 LLRKPNTPPKMIPEFCDT 380

#### RESULT 5

ID W24972 standard; Protein; 380 AA.

AC W24972;  
DT 22-JUN-1995 (first entry)  
DE Human interleukin-13 receptor.  
KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.  
OS Homo sapiens.  
FH key location/Qualifiers  
FT Peptide 1. 21  
FT /note- "signal peptide"  
PN W09723925-A1.  
PD 07-NOV-1996; F01756.  
PT 06-DEC-1995; FR-014424.  
PA (SMK-) SANOFI SA.  
PI Lepret D, Ferrara P, Laurent P, Vita N;  
PI MPI: 97-319773/29.  
DR N-PSDB: T85826, T86464.  
PT New purified human interleukin-13 receptors - and related nucleic  
PT acids, useful for diagnosis and treatment of inflammation, allergy,  
PT etc  
PS Claim 1; Figure 2a; 83pp; French  
CC This sequence represents interleukin-13 (IL-13) beta receptor. The  
CC invention relates to new purified peptides comprising 380 or 427 amino  
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
CC affinity, but acquires high affinity when associated with the IL-4

receptor. Nucleic acids encoding IL-13R beta and alpha are used as diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant IL-13R beta and alpha which can be used as IL-13 antagonists, specifically to regulate IL-13-induced responses for treatment of inflammation and allergy. IL-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-13R). Antibodies are used (in standard immunoassays) to diagnose diseases associated with abnormal expression of IL-13 receptors; when coupled to a toxin also for treatment of overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R. Note: IL-13R beta is encoded by the nucleic acid sequence shown in Figure 2a in the CC specification (T86464), which is not the same as that shown in the CC sequence listing (T85828).

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8, 1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAVVCAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
1 MAVVCAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
61 HFEKCTVEYELKRNIGSETWKTIIITKNLHYKDFLNGIEAKIHTLLPWQCTNGSEVQ 120  
61 HFEKCTVEYELKRNIGSETWKTIIITKNLHYKDFLNGIEAKIHTLLPWQCTNGSEVQ 120  
121 SSAEETWYISPGIPEIKYQDMDCVYNNQYLLCSMKPGIGVLDNTNLFYWEGLDH 180  
121 SSAEETWYISPGIPEIKYQDMDCVYNNQYLLCSMKPGIGVLDNTNLFYWEGLDH 180  
181 ALQCVYIRKADGNICRPFYLEASDYPKDFYICVNGSSEKPRSSYFTQLONYKPLP 240  
181 ALQCVYIRKADGNICRPFYLEASDYPKDFYICVNGSSEKPRSSYFTQLONYKPLP 240  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDYEIEIREDDTLVTAVENETYLKTNE 300  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDYEIEIREDDTLVTAVENETYLKTNE 300  
301 TROLCFVRSKVNIVYCSDDGIMSEWSDKOCWGEDLSKRTLLRFWLPFGIILLIVFTVG 360  
301 TROLCFVRSKVNIVYCSDDGIMSEWSDKOCWGEDLSKRTLLRFWLPFGIILLIVFTVG 360  
361 LLARKNTYPKMIPEFFCDT 380  
361 LLARKNTYPKMIPEFFCDT 380

RESULT 6  
ID W41520 standard; Protein: 380 AA.  
AC W41520;  
DT 22-JUN-1998 (first entry)  
DE Human HR-1 receptor.  
KW HR-1 receptor; human; cytokine; infection; asthma; allergy;  
KW haematopoietic disorder; tumour; therapy; diagnosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT Protein /label= Sfg\_peptide  
FT Protein /label= Mat\_protein  
PD WO9747741-A1.  
PD 18-DEC-1997.  
PE 12-JUN-1996; U10262.  
PR 12-JUN-1996; WO-010262.  
PA (HUMA-) HUMAN GENOME SCI. INC.  
PA (SMK-) SMITHKLINE BEECHAM CORP.  
PI Appelbaum ER, Hu J;  
DR WPI: 98-052308/05.

N-PSDB; V04131.  
Nucleic acid sequence encoding human cytokine peptide hormone receptor - useful to treat, prevent or diagnose, e.g. lowered resistance to infection, asthma, allergy or haematopoietic disease  
PS Claim 13; Page 62-64; 76pp; English.  
This protein comprises a novel human cytokine/peptide hormone receptor, designated the HR-1 receptor, that shows 27% identity and 52% similarity to the interleukin-5 receptor. Its amino acid sequence was deduced from a cDNA clone (see V04131) obtained from a human testis library. Recombinant HR-1 receptor can be expressed in claimed host cells, and used in a claimed method for identifying compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be used to treat, prevent or CC diagnose predisposition to lowered resistance to infection, asthma, CC allergic or haematopoietic disorders, e.g. where induced by AIDS, CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer. CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can be used to treat conditions associated with HR-1 receptor CC overexpression. The antibodies can also be used to determine HR-1 CC receptor levels, since overexpression may be diagnostic of tumours.  
SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8, 1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAVVCAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
1 MAVVCAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
61 HFEKCTVEYELKRNIGSETWKTIIITKNLHYKDFLNGIEAKIHTLLPWQCTNGSEVQ 120  
61 HFEKCTVEYELKRNIGSETWKTIIITKNLHYKDFLNGIEAKIHTLLPWQCTNGSEVQ 120  
121 SSAEETWYISPGIPEIKYQDMDCVYNNQYLLCSMKPGIGVLDNTNLFYWEGLDH 180  
121 SSAEETWYISPGIPEIKYQDMDCVYNNQYLLCSMKPGIGVLDNTNLFYWEGLDH 180  
181 ALQCVYIRKADGNICRPFYLEASDYPKDFYICVNGSSEKPRSSYFTQLONYKPLP 240  
181 ALQCVYIRKADGNICRPFYLEASDYPKDFYICVNGSSEKPRSSYFTQLONYKPLP 240  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDYEIEIREDDTLVTAVENETYLKTNE 300  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDYEIEIREDDTLVTAVENETYLKTNE 300  
301 TROLCFVRSKVNIVYCSDDGIMSEWSDKOCWGEDLSKRTLLRFWLPFGIILLIVFTVG 360  
301 TROLCFVRSKVNIVYCSDDGIMSEWSDKOCWGEDLSKRTLLRFWLPFGIILLIVFTVG 360  
361 LLARKNTYPKMIPEFFCDT 380  
361 LLARKNTYPKMIPEFFCDT 380

RESULT 7  
ID W36614 standard; Protein: 380 AA.  
AC W36614;  
DT 30-MAR-1998 (first entry)  
DE Human zcytor2 cytokine receptor protein.  
KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT Protein /label= Sfg\_peptide  
FT Protein /label= Mat\_protein  
PD WO9733913-A1.  
PD 18-SEP-1997.  
PE 12-MAR-1997; U04043.  
PR 13-MAR-1996; US-013345.  
PA (ZYMO-) ZYMOGENETICS INC.  
PA Baumgartner JW, Fairrah TM, Foster DC, Grant FJ,  
PI Ohara PJ;  
DR WPI: 97-470820/43.

DR N-PSDB; T96783.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Claim 1: Page 51-53; 79pp: English.  
 CC This sequence represents a novel, ligand-binding receptor, Zcytor2, which  
 CC shares homology with cytokine receptors and was isolated from a human  
 CC testis cDNA library. The resulting polypeptide is a receptor for  
 CC cytokines (particularly interleukin-13) and is expressed on the surface  
 CC of testicular cells, probably being involved in spermatogenesis. It can  
 CC be used to detect ligands that promote proliferation and/or  
 CC differentiation of such cells in cultures and may also be used to treat  
 CC infertility. Antagonists of this receptor may be used to characterise  
 CC ligand-receptor interactions and as male-specific contraceptives. By  
 CC blocking the action of IL-13, receptor antagonists and ligand-binding  
 CC this receptor can also be used to modulate immune function, e.g. in  
 CC allergy and asthma, as a diagnostic to determine circulating levels of  
 CC ligand and also to isolate and purify ligands. Antibodies can be used to  
 CC assay circulating receptor (an abnormal level may be indicative of  
 CC disease such as cancer), for labelling cells that express the receptor,  
 CC and therapeutically as antagonist.  
 SO Sequence 380 AA.

Query Match 98.8%; Score 2078; DB 1; Length 380;  
 Best Local Similarity 99.2%; Pred. No. 2,5e-191;  
 Matches 377; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGGCTSSSDTEIKVNPDPFEYDPEYLGVLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTLSTTGGCTSSSDTEIKVNPDPFEYDPEYLGVLQWQPPSLD 60  
 QY 61 HFEKCTVEYELKRNISEETWKTITITKLNHYKQGFDLNKGIEAKIHTLLPMQNGSEVQ 120  
 DB 61 HFEKCTVEYELKRNISEETWKTITITKLNHYKQGFDLNKGIEAKIHTLLPMQNGSEVQ 120  
 QY 121 SSMATETWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 DB 121 SSMATETWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 QY 181 ALOCVDYIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 DB 181 ALOCVDYIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 QY 241 PVLITFRESSCEIKLWMSIPIGIPARCFDYIEIREDDTLTAVAVENTYTLKTNE 300  
 DB 241 PVLITFRESSCEIKLWMSIPIGIPARCFDYIEIREDDTLTAVAVENTYTLKTNE 300  
 QY 301 TROLCEVRSKVNIIYCSDDGIMSEMSDKOCWEGEDLSKTLRLFWLPFGFILLIVFVVG 360  
 DB 301 TROLCEVRSKVNIIYCSDDGIMSEMSDKOCWEGEDLSKTLRLFWLPFGFILLIVFVVG 360  
 QY 361 LLRKRPNTYPKMIPFPCDT 380  
 DB 361 LLRKRPNTYPKMIPFPCDT 380

RESULT 8  
 W36616  
 ID W36616 standard; Protein; 372 AA.

AC W36616;  
 DT 30-MAR-1998 (first entry)  
 DE Celebus macaque zcytor2 protein.  
 KM Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 KW Infertility; antagonist; contraceptive; diagnostic; therapeutic.  
 OS Macaque sp.  
 FH Key  
 FT Location/Qualifiers  
 FT 1..372  
 FT /label= zcytor2  
 FT /note= "partial protein sequence"

PD MO9733913-AL  
 PD 18-SEP-1997  
 PF 12-MAR-1997; 004043.

PR 13-MAR-1996; 75-013345.  
 CC (Zymo) ZYM-GENETICS INC.  
 PT Bounded; JM, Farrah TM, Foster DC, Grant FT,  
 PT Charr PJ.  
 PS SPT; 97-470820/43.  
 DR N-PSDB; T96784.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Example 4: Page 56-57; 79pp: English.  
 CC This sequence represents a novel ligand-binding receptor, Zcytor2,  
 CC which shares homology with cytokine receptors and is isolated from  
 CC testis tissue obtained from a Celebus macaque. The resulting polypeptide  
 CC is a receptor for cytokines (particularly interleukin-13) and is  
 CC expressed on the surface of testicular cells, probably being involved in  
 CC spermatogenesis. It can be used to detect ligands promoting proliferation  
 CC and/or differentiation of such cells in cultures and may also be used to  
 CC treat infertility. Antagonists of this receptor may be used to  
 CC characterise ligand-receptor interactions and as male-specific  
 CC contraceptives. By blocking the action of IL-13, receptor antagonists and  
 CC ligand-binding this receptor can also be used to modulate immune  
 CC function, e.g. in allergy and asthma, as a diagnostic to determine  
 CC circulating levels of ligand and also to isolate and purify ligands.  
 CC Antibodies can be used to assay circulating receptor (an abnormal level  
 CC may be indicative of disease such as cancer), for labelling cells that  
 CC express the receptor, and therapeutically as antagonist.  
 SO Sequence 372 AA.

Query Match 88.1%; Score 1853; DB 1; Length 372;  
 Best Local Similarity 92.2%; Pred. No. 9.2e-170;  
 Matches 343; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGGCTSSSDTEIKVNPDPFEYDPEYLGVLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTLSTTGGCTSSSDTEIKVNPDPFEYDPEYLGVLQWQPPSLD 60  
 QY 61 HFEKCTVEYELKRNISEETWKTITITKLNHYKQGFDLNKGIEAKIHTLLPMQNGSEVQ 120  
 DB 61 HFEKCTVEYELKRNISEETWKTITITKLNHYKQGFDLNKGIEAKIHTLLPMQNGSEVQ 120  
 QY 121 SSMATETWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 DB 121 SSMATETWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 QY 181 ALOCVDYIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 DB 181 ALOCVDYIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 QY 241 PVLITFRESSCEIKLWMSIPIGIPARCFDYIEIREDDTLTAVAVENTYTLKTNE 300  
 DB 241 PVLITFRESSCEIKLWMSIPIGIPARCFDYIEIREDDTLTAVAVENTYTLKTNE 300  
 QY 301 TROLCEVRSKVNIIYCSDDGIMSEMSDKOCWEGEDLSKTLRLFWLPFGFILLIVFVVG 360  
 DB 301 TROLCEVRSKVNIIYCSDDGIMSEMSDKOCWEGEDLSKTLRLFWLPFGFILLIVFVVG 360  
 QY 361 LLRKRPNTYPKM 372  
 DB 361 LLRKRPNTYPKM 372

RESULT 9  
 W56260  
 ID W56260 standard; Protein; 359 AA.

AC W56260;  
 DT 16-SEP-1993 (first entry)  
 DE Construct containing mature interleukin-13 binding protein.  
 KM Therapeutic; IL-13 mediated condition; allergy; asthma; diagnosis;  
 KW autoimmune disease; antibody; immunotherapy.  
 OS Homo sapiens  
 FH W09810539-AL  
 PF 19-MAR-1993.

PF 10-SEP-1997; AU00591.  
 PR 27-FEB-1997; AU-005374.  
 PR 10-SEP-1996; AU-002262.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;  
 DR WPI: 98-207062/18.  
 DR N-PSDB: V22701.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PR products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection  
 PS Example 14: Page 52-53: 69pp; English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.  
 SO Sequence 359 AA;

Query Match 83.3%; Score 1753; DB 1; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 3, 4e-160;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDDFELVDPGILYLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTIIITKN 88  
 DB 45 EIKVNPDDFELVDPGILYLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTIIITKN 104  
 QY 89 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPEKVDMDCVY 148  
 DB 105 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPEKVDMDCVY 164  
 QY 149 NMOTLLCSMRPGIGVLDITNLYNFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 208  
 DB 165 NMOTLLCSMRPGIGVLDITNLYNFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 224  
 QY 209 DEYICVNGSSSEKPIRSSYFTFOLNIVKPLPYVILTFTRSSCEIKLWISPLGIPAR 268  
 DB 225 DEYICVNGSSSEKPIRSSYFTFOLNIVKPLPYVILTFTRSSCEIKLWISPLGIPAR 284  
 QY 269 CFDEYEIREDDTLLVATAVENETYLKTNETRQLCFVVRSKNIVYCSDDGIMSEMSDK 328  
 DB 285 CFDEYEIREDDTLLVATAVENETYLKTNETRQLCFVVRSKNIVYCSDDGIMSEMSDK 344  
 QY 329 QCWEGEDLSKTLIR 343  
 DB 345 QCWEGEDLSKTLIR 359

RESULT 10  
 ID W56261 standard; Protein; 315 AA.  
 AC W56261;  
 DT 16-SEP-1998 (first entry)  
 DE Mature interleukin-13 binding protein.  
 KW Therapeutic; IL-13 mediated condition; allergy; asthma; diagnosis;  
 KW autoimmune disease; antibody; immunotherapy.  
 OS Homo sapiens.  
 PN WO9810638-A1.  
 PD 19-MAR-1998.  
 PF 10-SEP-1997; AU00591.  
 PR 27-FEB-1997; AU-005374.  
 PR 10-SEP-1996; AU-002262.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;  
 DR WPI: 98-207062/18.  
 DR N-PSDB: V22702.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PR products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection  
 PS Disclosure; Page 55-56; 69pp; English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used

CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.  
 SO Sequence 315 AA;

Query Match 83.3%; Score 1753; DB 1; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 2, 8e-160;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDDFELVDPGILYLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTIIITKN 88  
 DB 1 EIKVNPDDFELVDPGILYLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTIIITKN 60  
 QY 89 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPEKVDMDCVY 148  
 DB 61 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPEKVDMDCVY 120  
 QY 149 NMOTLLCSMRPGIGVLDITNLYNFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 208  
 DB 121 NMOTLLCSMRPGIGVLDITNLYNFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 180  
 QY 209 DEYICVNGSSSEKPIRSSYFTFOLNIVKPLPYVILTFTRSSCEIKLWISPLGIPAR 268  
 DB 181 DEYICVNGSSSEKPIRSSYFTFOLNIVKPLPYVILTFTRSSCEIKLWISPLGIPAR 240  
 QY 269 CFDEYEIREDDTLLVATAVENETYLKTNETRQLCFVVRSKNIVYCSDDGIMSEMSDK 328  
 DB 241 CFDEYEIREDDTLLVATAVENETYLKTNETRQLCFVVRSKNIVYCSDDGIMSEMSDK 300  
 QY 329 QCWEGEDLSKTLIR 343  
 DB 301 QCWEGEDLSKTLIR 315

RESULT 11  
 ID W35294 standard; Protein; 383 AA.  
 AC W35294;  
 DT 27-MAR-1998 (first entry)  
 DE Murine IL-13 binding chain of the IL-13 receptor.  
 KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;  
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;  
 KW allergy; asthma; immune complex disorder.  
 OS Mus sp.  
 PN W09731946-A1.  
 PD 04-SEP-1997.  
 PF 28-FEB-1997; U03124.  
 PR 01-MAR-1996; US-609572.  
 PA (GENY) GENETICS INST INC.  
 PI Collins M, Donaldson D, Filtz L, Neben T, Whitters M,  
 DR WPI: 97-448632/41.  
 DR N-PSDB: T75213.  
 PT New nucleic acid encoding interleukin-13 receptor binding chain and  
 PT transformed cells - proteins, antibodies and inhibitors, for  
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
 PT and in diagnosis

PS Claim 11: Pages 30-31: 49pp; English.  
 CC The present sequence represents the murine interleukin-13 (IL-13) binding  
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a  
 CC mediator of the known biological activities of IL-13. Recombinant  
 CC IL-13bc proteins, and antibodies raised against them, are used to  
 CC inhibit the binding of IL-13 to its receptor. They are particularly used  
 CC to treat IIS-mediated conditions, e.g. allergy, asthma and immune complex  
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.  
 CC They are also used to treat immune deficiency (particularly in  
 CC hematopoietic progenitor cells), cancer etc., and to increase macrophage  
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  
 CC with such activity is combined with IL-13bc and the mixture applied,  
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor  
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect  
 CC expression of IL-13, its receptor or binding chain, and to raise specific  
 CC antibodies which may be useful for treating some tumours.  
 SQ Sequence 383 AA;

Query Match 56.8%; Score 1194.5; DB 1: Length 383;  
 Best Local Similarity 58.9%; Pred. No. 1.3e-106;  
 Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAVVLAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDGYLGYLQWQPLSLD 60  
 DB 1 MAVV--HIRCLFILLCTINGYS-----LEIKVNPPODFEILDGILGYLQWKPPIVIE 54  
 QY 61 HRECEVEYELKRNIGSETWKTITIKNLHKKGFDLKNKIEAKIHTLFPWCTNGSEVO 120  
 DB 55 KFGGCTLEVEYELKRNVDSDWKTITIRNLTKGFDLKNKIEKIRTHLSEHCTNGSEVO 114  
 QY 121 SSAETTYTSPGIDETKVDMDQVYNNQYLLCSMKPGIGVLDPNLYLFTWYBESLDH 180  
 DB 115 SPTEISYGISDSGSELETKIQDKMKCIYNNQYLYVCSMKPKRTYSIDNTYMFYBESLDH 174  
 QY 181 ALQCVDIYKADGONICRPFYLEASDYKDFYICVNGSSSENKPIRSSYFTPOLNTYKPLP 240  
 DB 175 ALQCAVYLDHDEKNVCKLSNLDSDYKDFEIVNGSSSKLEPIRSSYFTVQLQNTYKPLP 234  
 QY 241 PVLITFTRESSCEIKLWSIPLGPIPARCFDYIEIREDDTLVLTATVEVETTLTKTNE 300  
 DB 235 PEFLLHSIVSNSIDIRKMKWSPGPIPPRCYTYEIVIREDDISWESATDKMDMLKRRANE 294  
 QY 301 TRLQCVVSKVNIYCSDDGIMSEWSDKQWEGEDSKTKLLTFMPLFGFILLIVPVG 360  
 DB 295 SEDLCEYVCKKNVITCADGIMSEWSEECWEGYTGPDCKIT-FIVPVCLFFILLLLLC 353  
 QY 361 LLRKRPNTYPKM 372  
 DB 354 LIVEKEPEPTL 365

RESULT 12  
 ID W56252  
 AC W56252; standard; Protein: 157 AA.  
 DT 16-SEP-1998 (first entry)  
 DE Interleukin-13 binding protein N-terminal ORF 1.  
 KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;  
 KW autoimmune disease; antibody; immunotherapy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT MISC\_difference 6 /note= "Stop codon"  
 FT MISC\_difference 7 /label= "Unknown"  
 FT MISC\_difference 17 /note= "Encoded by gln"  
 FT MISC\_difference 17 /note= "Stop codon"  
 FT Peptide 44..68  
 FT /note= "Putative signal sequence"  
 FT MISC\_difference 141 /label= "Unknown"  
 FT

F4 /note= "Encoded by cmt"  
 F4 MISC\_difference 142 /note= "Stop codon"  
 FT W09910638-21  
 F4 19-MAR-1998  
 F4 10-SEP-1997; AV0591.  
 F4 27-FEB-1997; AV-005374.  
 PR 17-SEP-1996; AV-002262.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PJ Hilton DJ, Nicola MA, Simpson RJ, Zhang J;  
 DR WPI: 98-207062/18.  
 DR N-PSDB: V22697.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PT products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection.  
 PS Claim 7: Page 44: 68pp; English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.  
 SQ Sequence 357 AA;

Query Match 21.7%; Score 456; DB 1: Length 157;  
 Best Local Similarity 77.2%; Pred. No. 2.4e-36;  
 Matches 86; Conservative 10; Mismatches 12; Indels 4; Gaps 3;

QY 1 MAVVLAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDGYLGYLQWQPLSLD 60  
 DB 43 MAVVLAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDGYLGYLQWQPLSLD 102  
 QY 61 HRECEVEYELKRNIGSETWKTITIKNLHKKGFDLKNKIEAKIHTLFPWCTNGSEVO 110  
 DB 103 HRECEVEYELKRNIGSETWEGPILRIYIKGWGIDXXGALKAKVTHGFVP 156

RESULT 13  
 ID R22216  
 AC R22216; standard; Protein: 396 AA.  
 DT 22-JUL-1992 (first entry)  
 DE Sequence of human interleukin-5 receptor with signal peptide  
 DE (from a patient of eosinophilia).  
 KW Allergic disorder; therapy; eosinophilia.  
 OS Mouse.  
 F4 AF-475746-A;  
 F4 10-MAR-1992.  
 F4 11-SEP-1991; 308309.  
 F4 11-SEP-1990; DP-240638.  
 PA (TAKA) TAKATSU K.  
 F4 Takatsu K, Tomimaga A, Takagi S, Murata Y;  
 F4 WPI: 92-090329/12.  
 F4 Human and murine interleukin-5 receptor and DNA encoding them -  
 F4 for treatment of auto-immune and eosinophilia conditions  
 F4 involving IL-5.  
 PS Claim 21: Page 42-44: 65pp; English.  
 CC The inventors claim: an isolated cDNA sequence encoding murine  
 CC (secretory) interleukin-5 (IL-5) receptor, which is synthesised from  
 CC murine early P cell mRNA; an isolated murine (secretory) IL-5  
 CC receptor; an isolated cDNA sequence encoding human (secretory) IL-5  
 CC receptor, which is synthesised from mRNA of human peripheral blood  
 CC eosinophil; and an isolated human (secretory) IL-5 receptor. Also  
 CC claimed are a COS monkey cell transfected with a recombinant vector  
 CC contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a  
 CC transmembrane region; and an expression vector.  
 SQ Sequence 396 AA;

Query Match 14.8%; Score 311.5; DB 1: Length 396;  
 Best Local Similarity 26.6%; Pred. No. 6.2e-22;

	Matches	99;	Conservative	70:	Mismatches	156;	Indels	47;	Gaps	16;
OY	27	DTEIVNPPODEIYDPGLTYILQWOPPLSLDHFKECTVEYEELKYNISSETKTITTT	86	I : I :	:	:	:	:   :  :	:	:
Db	25	DEKISLLPVPNTTIKTG-LAOVLLQMKRNPDOEQ-RNVNLLEYOKINAPKKEDDETRTT	82	:: ::	:	:	:	:   :  :	:	:
OY	87	KMLHKDGFDLKNKGIEAKIHHTLPMQCTNGSEVOSSMAETTWISPQIPERKYODMOCV	146	:: ::	:	:	:	:   :  :	:	:
Db	83	ES---KCVTILLKHGSASVRTILO--NDHSLASSMASAEHL-APPSPGISYVALJTC	135	:: ::	:	:	:	:   :  :	:	:
OY	147	-----YYNMÖYL-CSMKPFGIGVLDDTNMYLF----WEGLIDHALQCVDYIKAD	191	:: ::	:	:	:	:   :  :	:	:
Db	136	TMTTEDNYSRLASYSQSLTMCLWGTDARDEDQIFLYIRSGSME-----ECQEISKPT	189	:: ::	:	:	:	:   :  :	:	:
OY	192	-GNICCRFP--YLEASDYKDFTYCANGSENENKRFSSTFFLOLNAYKLPPVIYLTFR	248	:: ::	:	:	:	:   :  :	:	:
Db	190	LGRNIACMPREFFIILSKRGMDLAFLVNCGSSKSHSARPQNQLALHAIDOINPELVTAEI	249	:: ::	:	:	:	:   :  :	:	:
OY	249	EASSECEKLMSPIPGIPARCDFEYEIEDDTITTAVENEPTYTLKNTNEFROLCFYV	308	:: ::	:	:	:	:   :  :	:	:
Db	250	EQT-FRIStOMEKVSAFPHCFDEYEKHNTRNGYIQIELKMTNAFISIIDDLSKIADVQ	308	:: ::	:	:	:	:   :  :	:	:
OY	309	RSKVINCYSDPDIVSEMSEDKOCCMGEGDLTSKTLRLRPFCFILII-----VFIEYTGL	362	:: ::	:	:	:	:   :  :	:	:
Db	309	RAAVSMCMGEAGIMWSMS-QPIYVGDNEMK-PLRBM-----FYIVAMATCIILLILSLI	361	:: ::	:	:	:	:   :  :	:	:
OY	363	LRRPNTYPRMPI	374	:	:	:	:	:	:	:
Db	362	CXCHLMIKLFP	373	:	:	:	:	:	:	:
	RESULT	14								
ID	R22219	R22219 standard; Protein: 420 AA.								
AC	R22219;									
DI	22-JUL-1992	(first entry)								
DE	Sequence of secretory interleukin 5 receptor (HSIU-5R).									
KM	Autoimmune disorder; therapy: eosinophilia.									
OS	Homo sapiens.									
FH	Key	Location/Qualifiers								
FH	peptide	1..20								
FT	/label= signal									
PB	EP-475746-A.									
PD	18-MAR-1992.									
PF	11-SEP-1991: 308309.									
PR	11-SEP-1990: JP-240638.									
PA	(TAKA/) TAKATSU K.									
PI	Takatsu K, Tomlinaga A, Takagi S, Murata Y,									
DR	NPSDB: Q22978.									
PT	Human and murine Interleukin-5 receptor and DNA encoding them -									
PR	for treatment of auto-immune and eosinophilla conditions									
PI	Involving IL-5									
PC	Dislosure: Page 49: 65pp: English.									
CC	The inventors claim: an isolated cDNA sequence encoding murine									
CC	(secretory) interleukin-5 (IL-5) receptor, which is synthesised from									
CC	murine early B cell mRNA; an isolated murine (secretory) IL-5									
CC	receptor; an isolated cDNA sequence encoding human (secretory) IL-5									
CC	receptor, which is synthesised from mRNA of human peripheral blood									
CC	eosinophil; and an isolated human (secretory) IL-5 receptor. Also									
CC	claimed are a COS monkey cell transfected with a recombinant vector									
CC	contg. The DNA: secretory human IL-5 lacking a cytoplasmic and a									
CC	transmembrane region; and an expression vector.									
SQ	Sequence 420 AA;									
OY	Query Match	14.8%;	Score 311.5;	DB 1;	Length 420;					
	Best Local Similarity	26.9%;	Pred. No. 6.8e-22;							
	Matches 100;	Conservative 69;	Mismatches 156;	Indels 47;	Gaps 16;					
OY	27 DREIVNPPODEIYDPGLTYILQWOPPLSLDHFKECTVEYEELKYNISSETKTTT	86	I : I :	:	:	:	:   :  :	:	:	
Db	25 DEKISLLPVPNTTIKTG-LAOVLLQMKRNPDOEQ-RNVNLLEYOKINAPKKEDDETRTT	82	:: ::	:	:	:	:~::~	:	:	

```

0Y 87 KILHAKDGFDLNKKGEAKHHTLTPMOCNTNGSSVSSMAETTWISPOGIPERKYDMDCV 146
Db 83 ES---KCVTILHKKGSASVRIILQ---NDHSLTASSMSAEIHL-APPGSPGTSVNLITCT 135
0Y 147 -----YNNMOYLL-CSWKPPIGVLLDNTNVLFY---WYEGDLHALOCVDYIKAD 191
Db 136 TWITEDTNSRLSSQVSLHCTWLVTGIDAPEDIQYFLFYRSGWTE-----ECQFSKDT 189
0Y 192 -GQNGICRPP--YLEASDYKDFYICVNGSSSEKKPIRSSFTTQLONIYKPLPVLITFR 248
Db 190 IGRNATCEPPTPIILSKGRDWLAVLVNSSKSHALRPDQFLALAIQDINPLVMTAEI 249
0Y 249 ESSCEIKLWMSIPLPIPARCFDEYIEIRREDDTLTVAATENETYLTKTNTFPOLCFV 308
Db 250 EST-RLSLQMEKPVSAFPHCFDYEVKLIHNRNGLIQLEKLTNAFISLIIDLSKIDQV 308
0Y 309 RSKVNIYSDSDGIMSEWSDKOCMEGEDLSKTLTFWLPFGFILL-----VIEVTGLL 362
Db 309 RAIVSSMCREALGMEWS-QPIYVGNDEHKP--LREW-----FVIYIMATICPILLISLI 361
0Y 363 LKRPNTYKRMIP 374
Db 362 CKICHLMIKLPF 373

RESULT 15
R22220
ID R22220 standard: Protein; 396 AA.
AC R22220.
DT 22-JUL-1992 (first entry)
DE Sequence of secretory interleukin 5 receptor (HSIL-5R2).
OS Autoimmune disorder: therapy; eosinophilia.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..20
FT /label=signal
PE EP-475746-A.
PD 18-MAR-1992.
PF 11-SEP-1991; 308309.
PR 11-SEP-1990; JP-240638.
PA (TAKA/) TAKATSU K.
PJ Takatsu K, Tomimaga A, Takagi S, Murata Y;
DR N-PSDB; Q22979.
DR Human and murine interleukin-5 receptor and DNA encoding them -
PI for treatment of auto-immune and eosinophilia conditions
PT Involving IL-5
PS Disclosure: Page 51; 65pp; English.
CC The inventors claim: an isolated cDNA sequence encoding murine
CC (secretory) interleukin-5 (IL-5) receptor, which is synthesised from
CC murine early B cell mRNA; an isolated murine (secretory) IL-5
CC receptor; an isolated cDNA sequence encoding human (secretory) IL-5
CC receptor, which is synthesised from mRNA of human peripheral blood
CC eosinophils; and an isolated human (secretory) IL-5 receptor. Also
CC claimed are a COS monkey cell transfected with a recombinant vector
CC contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a
CC transmembrane region; and an expression vector.
SD Sequence 396 AA.

Query Match 14.8%; Score 311.5; DB 1; Length 396;
Best Local Similarity 26.9%; Pred. No. 6, 2e-22;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

0Y 27 DIEIVANPPODEIYDGLGLYLIQOMPPLSLDFKCECTVEYELKYNRIGSETWKTIT 86
Db 25 DEKISLPLPVNTEIKYTG-IAQVLLQMKRPNPOEO-RUNVNLEYQVKNAPKDEDEYTRIT 82
0Y 87 KILHAKDGFDLNKKGEAKHHTLTPMOCNTNGSSVSSMAETTWISPOGIPERKYDMDCV 146
Db 83 ES---KCVTILHKKGSASVRIILQ---NDHSLTASSMSAEIHL-APPGSPGTSVNLITCT 135

```

QY 147 -----YNNQYLL-CSMRPGIGVLLDTNNLPY-----WYEGJDAHALQCVYIKAD 191  
 Db 136 TMTEDNYSRLRSYQVSLHCTWLVGTFDAPEDTOYFLYRGSWTE-----ECQEYSKDT 189  
 QY 192 -GONIGCRP--YLEASDYKDFIICVNGSSSENKPIRSSYTFQLONYVKPLPPYLLFTFR 248  
 Db 190 LGRNICWEPFRFTILSKGRDMLAVLVNGSSKSHAIRPFDOLFALHAIDQINPPLNTAEI 249  
 QY 249 ESSCEIKLKSIPUGPIPARCFDEIEIRDDDTLVTAIVENETYLKTNETFQLCFVY 308  
 Db 250 EGT-RLSIQWKEKVSAPFHCDFEYVAKIHNTKNGYLOIEKIMTNAFISIIDDLSKYDVQV 308  
 QY 309 RSKVNIYCSDDGIWSEWSDRQCEGEDLSKRTLLRFWLPFGFILL-----VIFVTGL 362  
 Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREM-----FVIVIMATICFILLISLI 361  
 QY 363 LRKPNTYPMIP 374  
 Db 362 CKICHLMIKLFP 373

Search completed: January 19, 2000, 20:00:50  
 Job time: 8945 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 19, 2000, 13:58:11 ; Search time 71.05 seconds  
(without alignments)  
252.278 Million cell updates/sec

Title: US-09-077-817-2  
Perfect score: 2104  
Sequence: 1 MAFVCLAIQCLYFLISTF.....LLLRKPNTYPMIPEFCDT 380

Scoring table: BLOSUM62

Searched: 142080 segs, 47169319 residues

Database: PIR\_62:\*

Word size: 0

Number of hits that pass the threshold: 142080

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	311.5	14.8	420	2	S21052	interleukin-5 rece
2	311.5	14.8	396	2	S21050	interleukin-5 rece
3	293	13.9	333	2	S21053	interleukin-5 rece
4	292	13.5	335	2	A40267	interleukin-5 rece
5	263	12.9	831	2	J01655	prolactin receptor
6	247	11.7	415	2	S12357	interleukin-5 rece
7	220	10.5	369	2	A42565	interleukin-2 rece
8	216.5	10.3	830	2	IS0455	prolactin receptor
9	212.5	10.1	369	2	IA9280	interleukin-2 rece
10	208	9.9	373	2	A57118	interleukin-2 rece
11	195	9.3	878	1	A40091	interleukin-3 rece
12	180.5	8.6	897	1	A39255	cytokine receptor
13	178	8.5	896	1	IS5653	interleukin-3 rece
14	173.5	8.2	896	1	A35782	cytokine receptor
15	165	7.8	581	2	IA5971	prolactin receptor
16	165	7.8	610	2	A34631	prolactin receptor
17	165	7.8	610	2	A36116	prolactin receptor
18	165	7.8	412	2	A41070	prolactin receptor
19	165	7.8	310	2	A29884	prolactin receptor
20	160.5	7.6	303	2	IA7524	prolactin receptor
21	159	7.6	282	2	IA7525	prolactin receptor
22	159	7.6	608	2	IA5269	prolactin receptor
23	151	7.2	206	2	A57018	prolactin receptor
24	151	7.2	622	2	A40144	prolactin receptor
25	150.5	7.2	917	2	IA9699	glycoprotein 130 -
26	149	7.1	616	2	A30304	prolactin receptor
27	142.5	6.8	400	2	S06945	granulocyte-macrop
28	138	6.6	378	2	A40266	granulocyte-macrop
29	134.5	6.4	1097	2	IA7308	leukemia inhibitor
30	133.5	6.3	333	2	S13684	granulocyte-macrop
31	133.5	6.3	378	2	S50040	granulocyte-macrop
32	131.5	6.2	630	2	IS1086	prolactin receptor
33	129	6.1	150	2	B34631	lactogen receptor
34	126.5	6.0	918	2	A36337	membrane glycoprot
35	122.5	5.8	286	2	S50039	granulocyte-macrop

36	120.5	5.7	783	2	JH0329	granulocyte colony
37	120.5	5.7	771	2	B38252	granulocyte colony
38	120.5	5.7	863	2	C38252	granulocyte colony
39	112.5	5.3	1630	2	C41214	protein-tyrosine-p
40	111.5	5.3	1557	2	D41214	protein-tyrosine-p
41	110	5.2	6805	2	S20901	titin - rabbit (fr
42	109.5	5.2	26926	1	I38344	titin, cardiac mus
43	109.5	5.2	918	2	A44257	interleukin-6 sign
44	107.5	5.1	638	2	A33991	somatotropin recep
45	107.5	5.1	638	2	S04530	somatotropin recep

ALIGNMENTS

```

RESULT 1
S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5r.12), membrane-anchored
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Feb-1998
C:Accession: S21052; A46175
R:Morata, Y., Takaki, S., Magita, M., Kikuchi, Y., Tomlinaga, A., Takatsu, K.
T: Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815
A:Accession: S21052
A:Molecule type: DNA
A:Accession: 1-420 <MUR>
A:Cross-references: EMBL:X61176; NID:933943; PID:933844
A:Experimental source: HL-60 cells and eosinophils
A:Experimental source: T. Tuyen, T. Placitnick, G. Verhee, A. Fiers, W. Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum
A:Reference number: A46175; MUID:92357767
A:Accession: A46175
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 333-420 <TAV>
A:Note: sequence extracted from NCBI database (NCBI:116243, NCBI:116244)
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; Transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-420/Domain: interleukin-5 receptor alpha chain #status predicted <MAT>
F:335-365/Domain: transmembrane #status predicted <TM>
F:335-337,137,142,216,244/Binding site: carbohydrate (asn) (covalent) #status predicte

Query Match 14.8% Score 311.5; DB 2; length 420;
East local similarity 26.9%; Pred. No. 2.3e-17;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

OY 27 DFEKVNPPQPELVDPYGLYLQWOPPLSLDFKCEYELKYNISSEKTIIT 86
DB 25 DEKISLPAPVNFITKVTG-LAQVLLQWKPNDQO-RVNVLEYQVKINAPREDEYERIT 82
OY 87 KNLHYKDFGDKGFEAKIHTLLPMOCNGSEVOSSNAETTYWSPOGIPETKVDMDCV 146
DB 83 ES--KCTYILHKGFSASVRIILO---NDHSLASSMASAEIH-APPSPTSIVNLTCT 135
OY 147 -----YNNQCYLL-CSMKPGIGVLLDTNNTLFY---WTEGDLHALQCVYIKAD 191
DB 136 TITFEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGSWE-----ECQYSKDT 189
OY 192 -CGNIGCTP--YLEASDKFYICVNGSSNNKPRSSYFFQOLNLYKPLPYLITFR 248
DB 190 LGRNIACWFPPTFLISKGRDLAVLVNNGSKSAIRPDQALAHADQINPPLVTAEI 249
OY 749 ESSEIKFKWGISPLGIPARCFDEIREDDTLLVATVENETTLTKTETROLGCVV 308
DB 250 EGT-KLSIQWKEKPVSAPIHCFDEKIHNRNGYLQLEKMTNAFISITIDLSKYDVQV 308
OY 309 RSKVNIYCSDDGIWSEMSDKCPGEGEDLSKRTLLRFWLPFGFIIIL-----VIFVIGIL 362
DB 309 RSKVNIYCSDDGIWSEMSDKCPGEGEDLSKRTLLRFWLPFGFIIIL-----VIFVIGIL 362

```

DB 309 RAAVSMCREAGIMSEMS-QPIYVGNDEHKP--LREM---FVIYIMATICFILLILSLI 361  
 OY 363 LRKPNTPPKMP 374  
 DB 362 CKICHIMIKLFP 373

## RESULT 2

S21050  
 Interleukin-5 receptor alpha chain precursor (clone lambda h5R.27) - human  
 C.Species: Homo sapiens (man)  
 C.Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 05-Jun-1998  
 C.Accession: S21050; S78106  
 R.Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.  
 J. Exp. Med. 175, 341-351, 1992  
 A.Title: Molecular cloning and expression of the human interleukin 5 receptor.  
 A.Reference number: S21050; MUID:92121815  
 A.Accession: S21050  
 A.Molecule type: DNA  
 A.Residues: 1-396 <MUR>  
 A.Cross-references: EMBL:X61177; NID:q33839; PID:q33840  
 A.Experimental source: clone lambda h5R.27  
 R.Murata, Y.  
 submitted to the EMBL Data Library, July 1991  
 A.Reference number: S78106  
 A.Accession: S78106  
 A.Molecule type: DNA  
 A.Residues: 1-128, '1', 130-396 <MUM>  
 A.Cross-references: EMBL:X61177; NID:q33839; PID:q33840  
 C.Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
 F:1-20/Domain: signal sequence #status predicted <Sig>  
 F:21-396/Product: interleukin-5 receptor alpha chain #status predicted <MAT>  
 F:345-365/Domain: transmembrane #status predicted <TM>  
 F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.8%; Score 311.5; DB 2; Length 396;  
 Best Local Similarity 26.9%; Pred. No. 2, 2e-17;  
 Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

OY 27 DPEIKNPDPDEIVDPGLYLYLWOMOPPLSDHFKCEVELEKRYNIGSTWTTIT 86  
 DB 25 DEKISLPVNFIFIKYTG-LAOVLLQMKRPNPDEQ-RNVNLEQVKNAPKEDYETRT 82  
 OY 87 KNLHYKGFGLNKIGIAKIHITLLPMQCTNGSEVOSSMAETTYWISPGGIPETKVDMDCV 146  
 DB 83 ES---KCVIILKHGFSASRTILQ---NDHSLASSMAAEHL-APPGSGISVNVLTCT 135  
 OY 147 -----YNNWOYLL-CSMKPGIGVLLDTNYNLFY---WYEGLDHALOCVDYIKAD 191  
 DB 136 TWTEDNYSRLSYQVSLHCTWLVGTDAPEDTQYFLYRGSWTE-----ECQERSKDT 189  
 OY 192 -GONIGCRPP--YLEASDKNDYICVNGSSEKPISSFTPOLQNTVPLPPLYLTFR 248  
 DB 190 LGRNACWPRFFIILSKGDMALAVLVNGSSKSHARPDLALHAIIDQINPLANTAEI 249  
 OY 249 ESSCEIKLKMSIPLPARPCEYEIEIRDDTTVATVENVETYLKTNERTROLCPVY 308  
 DB 250 EGT-RLSIQMERVSAFPHCFEYEVKINTRNGYLIQIEKMTNATISIIDLSKIDVQY 308  
 OY 309 RSKVNITCSDDGIMSEMSQKQEGEDLSKTLRLFWLPFGFILL-----VIFVTGLT 362  
 DB 309 RAAVSMCREAGIMSEMS-QPIYVGNDEHKP--LREM---FVIYIMATICFILLILSLI 361  
 OY 363 LRKPNTPPKMP 374  
 DB 362 CKICHIMIKLFP 373

## RESULT 3

S21053  
 Interleukin-5 receptor precursor soluble (clone lambda h5R.25) - human  
 C.Species: Homo sapiens (man)

C.Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 20-Feb-1998  
 C.Accession: S21053; S78107  
 R.Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.  
 J. Exp. Med. 175, 341-351, 1992  
 A.Title: Molecular cloning and expression of the human interleukin 5 receptor.  
 A.Reference number: S21050; MUID:92121815  
 A.Accession: S21053  
 A.Molecule type: mRNA  
 A.Residues: 1-333 <MUR>  
 A.Cross-references: EMBL:X62156; NID:q36465; PID:q36466  
 A.Experimental source: clone lambda h5R.25  
 R.Murata, Y.  
 submitted to the EMBL Data Library, September 1991  
 A.Reference number: S78107  
 A.Accession: S78107  
 A.Molecule type: mRNA  
 A.Residues: 1-128, '1', 130-333 <MUM>  
 A.Cross-references: EMBL:X62156; NID:q36465; PID:q36466  
 C.Keywords: alternative splicing; cytokine receptor; glycoprotein  
 F:1-20/Domain: signal sequence #status predicted <Sig>  
 F:21-333/Product: interleukin-5 receptor #status predicted <MAT>  
 F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.9%; Score 293; DB 2; Length 333;  
 Best Local Similarity 28.3%; Pred. No. 5, 1e-16;  
 Matches 90; Conservative 55; Mismatches 139; Indels 34; Gaps 12;

OY 27 DPEIKNPDPDEIVDPGLYLYLWOMOPPLSDHFKCEVELEKRYNIGSTWTTIT 86  
 DB 25 DEKISLPVNFIFIKYTG-LAOVLLQMKRPNPDEQ-RNVNLEQVKNAPKEDYETRT 82  
 OY 87 KNLHYKGFGLNKIGIAKIHITLLPMQCTNGSEVOSSMAETTYWISPGGIPETKVDMDCV 146  
 DB 83 ES---KCVIILKHGFSASRTILQ---NDHSLASSMAAEHL-APPGSGISVNVLTCT 135  
 OY 147 -----YNNWOYLL-CSMKPGIGVLLDTNYNLFY---WYEGLDHALOCVDYIKAD 191  
 DB 136 TWTEDNYSRLSYQVSLHCTWLVGTDAPEDTQYFLYRGSWTE-----ECQERSKDT 189  
 OY 192 -GONIGCRPP--YLEASDKNDYICVNGSSEKPISSFTPOLQNTVPLPPLYLTFR 248  
 DB 190 LGRNACWPRFFIILSKGDMALAVLVNGSSKSHARPDLALHAIIDQINPLANTAEI 249  
 OY 249 ESSCEIKLKMSIPLPARPCEYEIEIRDDTTVATVENVETYLKTNERTROLCPVY 308  
 DB 250 EGT-RLSIQMERVSAFPHCFEYEVKINTRNGYLIQIEKMTNATISIIDLSKIDVQY 308  
 OY 309 RSKVNITCSDDGIMSEMS 326  
 DB 309 RAAVSMCREAGIMSEMS 326

## RESULT 4

A40267  
 Interleukin-5 receptor alpha chain precursor - human  
 C.Species: Homo sapiens (man)  
 C.Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 10-Sep-1997  
 C.Accession: A40267  
 R.Savarnier, J.; Devos, R.; Cornelis, S.; Tuyenens, T.; Van der Heyden, J.; Piers, W.;  
 Celis, E.; 1175-1184, 1991  
 A.Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-sp  
 A.Reference number: A40267; MUID:92005669  
 A.Accession: A40267  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-335 <TAV>  
 A.Cross-references: GB:M75914; NID:q186387; PID:q186388  
 C.Keywords: cytokine receptor; transmembrane protein

Query Match 13.9%; Score 292; DB 2; Length 335;  
 Best Local Similarity 28.0%; Pred. No. 6, 2e-16;

Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

OY 27 DTEIKNPPDEFIVDPGYLYLQMPPLSLDHFKECVEYELKRNIGSEWTKIIT 86  
 DB 25 DEKISLPPVNFYKVTG-LAQVLLQWKPNDPOEQ-RNVNLEQVKINAPREDYERIT 82  
 OY 87 KNLHYDGEDLNKIGIAKIHITLLPMOCTNGSEVOSSWAETTYWISPOGIPETKODMDCV 146  
 DB 83 ES---KCVILHKGFSASVITLQ---NDHSCLASSASAKELH-APGSPGTSIVNLCT 135  
 OY 147 -----YYMQLL-CSMRPGIGVLLDTNINLFY---WEGIDHALQCVDYKAD 191  
 DB 136 TATTEEDNYSRLRSYOVSLHCTMTLWGTDPADPTQYFLIYRYSWTE-----ECOEYSKDT 189  
 OY 192 -GONIGCRFP--VLEASDYKDFICVNGSSSENNKPIRSSYTFPOLQNTKPLPYLITFTR 248  
 DB 190 LGNNIACWEPRTILSLGRDMLSVLVNGSSKSHAIRFDOLFALHAIDQINPLPLVTAET 249  
 OY 249 ESSCEIKLAKSIPLGPIPARCFDEIEIRDDTTLVATVENEYTLTKTNETROLCFV 308  
 DB 250 EGT-RLSIQMEKRVSAFPICFDEYKINHTRNGYLOIEKLMNAFISIIDLSKIVOV 308  
 OY 309 RSKVNYICSDDGIMSEWS 326  
 DB 309 RAAVSSMCREAGIMSEWS 326

## RESULT 5

Query Match 12.5%; Score 263; DB 2; Length 831;  
 Best Local Similarity 26.4%; Pred. No. 3 8e-13;  
 Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

OY 18 TTFGCTSSDTEIKVN--PPDPE---IVDPG-----YLGVLQWQPLSL 59  
 DB 97 TTEINIVTATNEIGNSSDPQYDVATSIYQSPVNLLETKRSANIMYAMAKWSPPLA 136  
 OY 60 DHKECTVELEKRYNIGSTTKITITKNLHYKDGFDLNGIEAKIHTLLPMOCTNGSEV 119  
 DB 157 DASSNHLHYHELKIRKEKEWETI---SVGVQTOCKIN-LNAGMYVVOVRCITLDPGE 212  
 OY 120 QSSMAETTWISPOG-IPETKVDMDCVYVNMQYLLCSMRPGIGVLLDTNINLFYWEG 178  
 DB 213 WSMWSESRHLITLSPGSPKPTITIKRSPKEKTFQWMPGLDGHPTVITLLYSKEGE 272  
 OY 179 DHALQCVDYKADQNGICRFPYLEASDYKDFYICVNGSSSENNKPIRSSYTFPOLQNTK 238  
 DB 273 EGYVECPDY-RTAGPN-SCFYDKKHTSEFTIYNITVATNEMGSSSDPHYVDTYVOP 330  
 OY 239 LPPVYLITFRESCEIK-----LWMS-IPGLPIARCFDEYIEIR---EDDTITLVATVEN 230  
 DB 331 DPVAVNTLELKKPKINRKYLVLTWSEPLADVRSGLTLEYELRLKPEGEWETIFVGO 390

A:Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849  
 A:Experimental source: Kidney  
 A:Keywords: glycoprotein; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:23-831/Product: prolactin receptor #status predicted <MAT>  
 F:439-460/Domain: transmembrane #status predicted <TM>  
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covalent)

OY 25 -ETLEKNETROLCHVSVSKVNYICSD--GIMSESDKQCE-GEDELKTKILLREWL 346  
 DB 391 QIQYKMSLNPGRKYY-----IQHCKPDHGSMSSESENITQIINDRYADM-VWI 443  
 OY 367 PEGFT-LILVIFVTGILLKRPNTYRMP 374  
 DB 444 VLGLASSLILIMSWTMYLKGYNITFMLP 473

RESULT 6  
 E12357  
 Interleukin-5 receptor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Mar-1998  
 C:Accession: S12357  
 R:Takaki, S.; Tomimaga, A.; Hiroshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu  
 EMO J. 9, 4367-4374, 1990  
 A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.  
 A:Reference number: S12357; M0ID:91092260  
 A:Accession: S12357  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-415 <YAK>  
 A:Cross-references: GB:D90205; NID:g220465; PID:d1014936; PID:g220466  
 A:Keywords: cytokine receptor; transmembrane protein

## Query Match 11.7%; Score 247; DB 2; Length 415;

Best Local Similarity 24.6%; Pred. No. 3e-12;  
 Matches 91; Conservative 70; Mismatches 151; Indels 58; Gaps 18;

OY 34 PDDEFIVDPGYLYLQMPPLSLDHFKECVEYELKRNIGSEWTKIITKNLHYKD 93  
 DB 29 PPNVFTKATG-LAQVLLHMDPNPDEQ-RVDEIVKYNAPQEDYTRKIES---KC 83  
 OY 94 GFLNKGIEAKIHITLLPMOCTNGSEVOSSWAETTYWISPOGIPETKVDMDCVYV 150  
 DB 84 VTLHEGFASVTRILK---SHTTLASSWVSAEL-KAPGSPGTSVNTLCTHTVSS 139  
 OY 150 -----WQY-LIISMRPGIGVLLDTNINLFYWEGDHALQCVDYK-ADQNGICRFP- 201  
 DB 140 HTHLRPYQVSLRQTLWVGKNDAPEDTQYFLYIRGVILE--KCOEYSDALNRYTACWFP 197  
 OY 201 -VLEASDYKDFYICVNGSSSENNKPIRSSYTFPOLQNTKPLPYLITFRESCEIKLWS 259  
 DB 198 TRINSGFEDLAVHINSSRAAIKPPDQLSPALDQVNPNNVYELISN-SLYQWE 256  
 OY 260 TPLGPIARCFDEYIEIRDD-----TTLVATVENEYTLTKTNETROLCFV 308  
 DB 257 KPLSAPPDHGFENNELKIYNNKNHICKELIANKFISKIDVSTISQ-----V 305  
 OY 305 RSKVNYICSDDGIMSESDKQCEGDELKTKILLREW---LDFPILVIVTGLLR 364  
 DB 306 RAAVSSPCRRPGRMGWS-OPIVYKE--RKSIVE-WHLIVLPACAFVLLIF--SLICR 359  
 OY 365 KPNYTRKMP 374  
 DB 360 VCHLWTRLP 365

## RESULT 7

Query Match 12.5%; Score 263; DB 2; Length 831;  
 Best Local Similarity 26.4%; Pred. No. 3 8e-13;  
 Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

OY 18 TTFGCTSSDTEIKVN--PPDPE---IVDPG-----YLGVLQWQPLSL 59  
 DB 97 TTEINIVTATNEIGNSSDPQYDVATSIYQSPVNLLETKRSANIMYAMAKWSPPLA 136  
 OY 60 DHKECTVELEKRYNIGSTTKITITKNLHYKDGFDLNGIEAKIHTLLPMOCTNGSEV 119  
 DB 157 DASSNHLHYHELKIRKEKEWETI---SVGVQTOCKIN-LNAGMYVVOVRCITLDPGE 212  
 OY 120 QSSMAETTWISPOG-IPETKVDMDCVYVNMQYLLCSMRPGIGVLLDTNINLFYWEG 178  
 DB 213 WSMWSESRHLITLSPGSPKPTITIKRSPKEKTFQWMPGLDGHPTVITLLYSKEGE 272  
 OY 179 DHALQCVDYKADQNGICRFPYLEASDYKDFYICVNGSSSENNKPIRSSYTFPOLQNTK 238  
 DB 273 EGYVECPDY-RTAGPN-SCFYDKKHTSEFTIYNITVATNEMGSSSDPHYVDTYVOP 330  
 OY 239 LPPVYLITFRESCEIK-----LWMS-IPGLPIARCFDEYIEIR---EDDTITLVATVEN 230  
 DB 331 DPVAVNTLELKKPKINRKYLVLTWSEPLADVRSGLTLEYELRLKPEGEWETIFVGO 390

A:Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849  
 A:Experimental source: Kidney  
 A:Keywords: glycoprotein; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:23-831/Product: prolactin receptor #status predicted <MAT>  
 F:439-460/Domain: transmembrane #status predicted <TM>  
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covalent)

A:Residues: 1-369 <TRAX>  
 A:Cross-references: GB:D11086; NID:g303611; PIDN:BA01857.1; PID:dl002334; PID:g219890  
 A:Experimental source: MOLT beta lymphoid cells  
 A:Note: sequence extracted from NCBI backbone (NCIP:109167)  
 R:Nozuchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.  
 J. Biol. Chem. 268, 13601-13608, 1993  
 A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.  
 A:Reference number: A46591; MUID:93293887  
 A:Accession: A46591  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-369 <RES>  
 A:Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058  
 R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He  
 Hum. Mol. Genet. 2, 1099-1104, 1993  
 A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked  
 A:Reference number: I54332; MUID:94004847  
 A:Accession: I54332  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-369 <RE2>  
 A:Cross-references: GB:L19546; NID:g349631; PIDN:AA37524.1; PID:g349632  
 C:Genetics:  
 A:Gene: GDB:IL2RG; SCIDX1: IMD4  
 A:Cross-references: GDB:134807; OMIM:308380  
 A:Map position: Xq13.1-Xq13.1  
 A:Intons: 39/1, 90/2, 152/1, 198/3, 253/1, 285/2, 308/3  
 A:Note: defects are associated with an X-linked form of severe combined immunodeficiency  
 C:Superfamily: interleukin-2 receptor gamma chain  
 C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunodeficiency

Query Match 10.5%; Score 220; DB 2; Length 369;  
 Best Local Similarity 25.5%; Pred. No. 3.5e-10;  
 Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

QY 97 LKGIKAKHITLIPMCCTNGSE-VQSSMAETTYWISPGIPEKRVQDMCVYINMOYLIC 155  
 DB 19 LKGLMTLTIT-----PQNGEDTADFLTPTDLSVSTLPLEVOCFVNVEMMC 72  
 QY 156 SW-----KPGIGVLLDTVYNLFYWEGLDH--ALQCVIRKADGNGICRPFYLEASD 207  
 DB 73 TNNSSSEPP-----TNLTHTYWKNSNDKVKCSHLSFEELTSGCOLKKEHL 125  
 QY 208 KDFYICVNGSSSEKPIRSSYFTQLOINVKPLPYVLTFTRESSCEIKLWSIPLGPIPA 267  
 DB 126 QTFVVOLODPRE--PRQATQMLKQNLVTPMAPENLTLKLSQSLQELMNW--NRFLN 180  
 QY 268 RQEDYIEIRERD-DTLYLVATVE-NETYLKTNETROLCFVYRSKVNIVYCSDDGIMSEW 325  
 DB 181 HCLEHLVQRTDMDHSWTQSDVYRHRKFSLPVDGQKRYTFVRSSRNPLCGSAQHMSEW 240  
 QY 326 SDQKWEGEDLSKRTLLRFMLPGFILLIIVFYTG 360  
 DB 241 SHPIHW-GSNTSKEN-----PFLFALNAVVISVG 268

RESULT 8  
 150455  
 prolactin receptor - pigeon  
 C:Species: Columba livia (domestic pigeon)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 13-Sep-1996  
 C:Accession: I50455  
 R:Chen, X.; Horsman, N.D.  
 Endocrinology 135, 269-276, 1994  
 A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.  
 A:Reference number: I50455; MUID:94483267  
 A:Accession: I50455  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-830 <CHES>  
 A:Cross-references: EMBL:U07694; NID:g466381; PID:g466382

Query Match 10.3%; Score 216.5; DB 2; Length 830;  
 Best Local Similarity 24.4%; Pred. No. 1.9e-09;  
 Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

QY 18 TRPGCTSSDTEKVPPODFEIVDGYLG-----YIYIDM 53  
 DB 97 TTYNITVYMANNEIGSNS-----DQYVDVTSIVQDPAVNLSTETKTSASTTYLLAKW 150  
 QY 54 QPPLSLDHFEECTV-EYELKYRNIGSEFTWITTKNLHAKDGFGLNKGIKAKHITLLPMQ 112  
 DB 151 SPPPLADVTSNSHYVYKELRLKPEKEEMETV---SVGQYQYKVR-LQAGKYVVOVR 206  
 QY 113 CTNGSEVQSSMAETTYWISPG-IPEKRVQDMCVYINMOYLICSKWPGIYGLDTNYNL 171  
 DB 207 CVLDIGEMSWSESRHIIHPNGESPPEKPTIICRSEKETFCWKRPGSDGHPNTYTL 266  
 QY 172 FYTEGLDHALQCVDIKADGNGICRPFYLEASDVKDYICVNGSSSEKPIRSSITFQ 231  
 DB 267 LYSKEGEERYECPDY-KTAGPN-SCYFDKHTSEFTIYINITYKATNEIGSNVSDPLYVD 324  
 QY 232 LQNVKPLPVYLTFTRESSCEIK---LKWS-IPLGPIPA--RQDYETETREDDTLY 284  
 DB 325 VYIYQTDPPVNTLELKTIVNRKPIVLTWSPPLADYRSGLTIDYELRLKPEA--- 382  
 QY 285 TATVENETYLKTNETROLCFVY---RSKVNIVGSD--GIWSEWS-DKQWEGEDLS 337  
 DB 382 -----PEWETIFVQQTQYKMSLNGKKYIVQIHCKPDHGSWSMSLEKYLQIPTDR 436  
 QY 338 KTLIRFMLPGFILLIIVFY 358  
 DB 437 IKDMV-VWIIYGLSLICLY 456

RESULT 9  
 149280  
 interleukin-2 receptor gamma chain precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 23-Jul-1999  
 C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398  
 R:Cao, X.; Kozak, C.A.; Liu, Y.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993  
 A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R)  
 A:Reference number: A47514; MUID:93391374  
 A:Accession: I49280  
 A:Molecule type: DNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-369 <CAO>  
 A:Cross-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350  
 A:Accession: A47514  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <RE2>  
 A:Cross-references: DBJ:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068  
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Suganura, K.  
 Biochem. Biophys. Res. Commun. 193, 356-363, 1993  
 A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of fu  
 A:Reference number: JN0592; MUID:93377575  
 A:Accession: JN0592  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <KUM>  
 A:Cross-references: DBJ:D13565; NID:g403684; PIDN:BA02760.1; PID:dl003265; PID:g303  
 R: Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.  
 Gene 130, 303-304, 1993  
 A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.  
 A:Reference number: JN0775; MUID:93366191  
 A:Accession: JN0775  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <KOB>  
 A:Cross-references: GB:D13821; NID:g436045; PIDN:BA02974.1; PID:dl003480; PID:g43604  
 R:Chiu, R.K.; Dougherty, G.J.  
 submitted to the EMBL Data Library, October 1993



2/6 IREDDITLVIAT-VENETYTLKTIIN-----ETRQLCFV-VRSKVNIYCSDDGIWSE 324

A:Titl : Cloning and expression of a gene encoding an interleukin 3 receptor

A: Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein

A:Reference number: A35782; M0ID:90319131  
 A:Accession: A35782  
 A:Molecule type: mRNA  
 A:Residues: 1-896 <GOR>  
 A:Cross-references: GB:M34397; NID:9191821; PIDN:AAA7204.1; PID:9309101  
 C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor  
 C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology  
 C:Keywords: cytokine receptor; duplication; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>  
 F:23-441/Domain: extracellular #status predicted <EXT>  
 F:39-235/Domain: cytokine receptor homology <CRS1>  
 F:253-434/Domain: cytokine receptor homology <CRS2>  
 F:442-463/Domain: transmembrane #status predicted <TM>  
 F:464-896/Domain: intracellular #status predicted <INT>

Query Match 8.2%; Score 173.5; DB 1; Length 896;  
 Best Local Similarity 20.7%; Pred. No. 5.2e-06;  
 Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

QY 5 CLAIGLTYFLITSTFGCS-----SSDTIK-----VNPQDEIYDPIGLCY 48  
 DB 94 CVPRRCVIP---TRFSTINEDIYSFRPDSDLGIQLMPLAQNVPPLPRNVSISSSEDR 150  
 QY 49 LYLQMOPL---SLDHFKETVEYELKYNIGSEFWKTIITKN-----LHYKDGFDLNG 100  
 DB 151 FLEHWSVSLGDQVSWLSKDIIEFVAVKRL-QDSMEDASLHFSKQVFEKFLPLNS 209  
 QY 101 IEA-KIHT-LLPQCTNGSEVSSMAETTYWISPGIPEKVDMDCVYNNMOYLCSWK 158  
 DB 210 IYAPRYRTRLYPGSSISGR--PSRWSPDEAMDSQPG-DKAQPNOLQCFEFGIQLHCSWE 266  
 QY 159 PGIGVLIDNNYNLFYWEGLDHALOCVDYIK-ADGONI-----GCRPYLEASDYKDFYIC 213  
 DB 267 VMTQTGSVSFGFLYRPSAPAEKCSPVKPEPGASVTRYHCSLPVPEPSAHSGTYS 326  
 QY 214 VNGSENKPIRSSYFTFOLNIYKPLPPVYLFTFRSSCEIKLWSIFLGPAPRCFDE 273  
 DB 327 V-----KHLQCKFLMSYNIOMEPTLNLTKNRDS---YSLHMETQKMAYSFIEHTFQ 377  
 QY 274 IETREDTTLVATVEN--ETYLKTTNETRQLCFYVRKVNINICSDDGIMSEMSDKQW 331  
 DB 378 VOYKKKSDSEWSEKTNLDRASHMDLSOLEPDTYCARVAVKPISNYDGIMSKSEETW 437  
 QY 332 EGEDLSKTLIRFWLPGFILLIYIVTGILL 363  
 DB 438 K-TDWVWPTL--WT---VLIVFLITLL 461

RESULT 15  
 145971  
 prolactin receptor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: 145971  
 R:Scott, P.; Kessler, M.A.; Schuler, L.A.  
 M:Cell, Endocrinol. 89, 47-58, 1992  
 A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin  
 A:Reference number: 145971; M0ID:93446019  
 A:Accession: 145971  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-581 <SCO>  
 A:Cross-references: GB:L02549; NID:9163617; PID:9163618  
 C:Genetics:  
 A:Gene: PRLR

Query Match 7.8%; Score 165; DB 2; Length 581;  
 Best Local Similarity 31.3%; Pred. No. 1.4e-05;  
 Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;

QY 136 PFCVQDMDCVYNNMOYLCSNKPFGIGVLDITNLFYWEGLDHALOCVDYIKADGONI 195  
 DB 27 PFCVQDMDCVYNNMOYLCSNKPFGIGVLDITNLFYWEGLDHALOCVDYIKADGONI 195  
 QY 195 GCATPFLASDNDYDFICVNGSENKPIRSSYFTFOLNIYKPLPPVYLFTFRSSCEIK 255  
 DB 85 SCYFG:KHTSIMKMYVITVNAIOMGSISSDPLVHVATYVEPEPPANLLELKHEDRX 144  
 QY 256 ---LAKSIP-LGPAPRCF--DYEIEIEDDTTLVATVENET-YTLKTTN-ETROLCE 306  
 DB 145 PYIMIKSPPTMDVSGWFIIOYELRLKPERAT-----DWETHHTLQOLKINLKY 198  
 QY 307 VVSLVNIYCS-DDGIWSEMS 326  
 DB 199 GKYLQVIRCKPDHGYWSEMS 219

Search completed: January 19, 2000, 14:58:48  
 Job time: 3637 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 20, 2000, 06:18:23 : Search time 35.05 Seconds

(without alignments)  
315.340 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: 2104

Sequence: 1 MAFVCLAIICLYFLISTTF.....ILLRKPTPKMIPEFCDT 380

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database : SwissProt\_38.\*

Word size : 0

Number of hits that pass the threshold : 80000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	380	1132_HUMAN	Q14627 homo sapien
2	310.5	14.8	420	ILSR_HUMAN	Q01344 homo sapien
3	298	14.2	424	1131_MOUSE	O09030 mus musculu
4	295.5	14.0	427	1131_HUMAN	P78552 mus sapien
5	263	12.5	831	PRLR_CHICK	O04594 gallus gall
6	247	11.7	415	ILSR_MOUSE	P21183 mus musculu
7	238	11.3	831	PRLR_MELGA	O91094 meleagris g
8	220	10.5	369	CYRG_HUMAN	P31785 homo sapien
9	216.5	10.3	830	PRLR_COLTI	O90374 columba liv
10	212.5	10.1	369	CYRG_MOUSE	P34902 mus musculu
11	208	9.9	373	CYRG_CANFA	P40321 canis famill
12	195	9.3	878	ILB3_MOUSE	P26954 mus musculu
13	189.5	8.0	379	CYRG_BOVIN	O95118 bos taurus
14	178.5	8.5	897	CYRB_HUMAN	P32927 homo sapien
15	173.5	8.2	896	CYRB_MOUSE	P26955 mus musculu
16	165	7.8	581	PRLR_BOVIN	O28172 bos taurus
17	165	7.8	610	PRLR_RAT	P05710 rattus norv
18	159	7.6	608	PRLR_MOUSE	O08501 mus musculu
19	151	7.2	622	PRLR_HUMAN	P16471 homo sapien
20	150.5	7.2	917	ILB6_MOUSE	O00560 mus musculu
21	150	7.1	581	PRLR_CEREL	O28335 cervus elap
22	149	7.1	616	PRLR_RABIT	P14787 oryctolagus
23	142.5	6.8	400	GMCR_HUMAN	P15509 homo sapien
24	138	6.6	378	ILB3_HUMAN	P26951 homo sapien
25	134.5	6.4	1097	ILB6_HUMAN	P42702 homo sapien
26	131.5	6.2	630	PRLR_ORENT	O91513 oreochromis
27	126.5	6.0	918	ILB6_HUMAN	P40189 homo sapien
28	120.5	5.7	836	GMCR_HUMAN	O90962 homo sapien
29	113.5	5.4	1165	LEPR_HUMAN	P48357 homo sapien
30	112.5	5.3	1630	PTPL_DROME	P35992 drosophila
31	109.5	5.2	918	ILB6_RAT	P40190 rattus norv
32	107.5	5.1	837	GMCR_MOUSE	P40923 mus musculu
33	107.5	5.1	638	ILB6_HUMAN	P10912 homo sapien
34	107	5.1	634	GMCR_BOVIN	P79108 bos taurus
35	106	5.0	634	GMCR_SHEEP	O28575 ovis aries
36	105	5.0	511	VGIG_VSVO	P04884 vesicular s
37	104.5	5.0	1092	ILB6_MOUSE	P42703 mus musculu
38	102.5	4.9	638	ILB6_PIG	P19756 sus scrofa
39	101.5	4.8	638	ILB6_RABBIT	P19941 oryctolagus

47 99.5 4.7 1162 1 ILB6\_RAT Q62959 rattus norv  
31 99 4.7 507 1 ILB6\_MOUSE P14753 mus musculu  
3 99 4.7 538 1 ILB6\_RAT P16310 rattus norv  
13 98.5 4.7 1162 1 ILB6\_MOUSE P48356 mus musculu  
14 98 4.7 511 1 VGIG\_VSVO P04883 vesicular s  
45 97 4.6 1040 1 AKO1\_RAT P22063 rattus norv

## ALIGNMENTS

RESULT 1  
1132\_HUMAN STANDARD; PRT; 380 AA.  
AC Q14627; 300667;  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DT 15-JUL-1999 (rel. 38, Last annotation update)  
DE INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13  
DE BINDING PROTEIN).  
GV IL13RA2 OR IL13R.  
CS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Euteria; Primates; Catarrhini; Hominoidea; Homo.  
RN [1]  
R1 SEQUENCE FROM N.A.  
R2 TISSUE-RENAI CELL CARCINOMA;  
RX WELCHER; 96279273.  
RA CAPOT D., LAURENT P., KAGHAD M., LELINS J.M., LEFORT S., VITA N.,  
RA FERRARA P.,  
RA "Cloning and characterization of a specific interleukin (IL)-13  
RA binding protein structurally related to the IL-5 receptor alpha  
RA chain".  
RT J. Biol. Chem. 271:16921-16926(1996).  
RZ [2]  
R1 SEQUENCE FROM N.A.  
R2 TISSUE-TESTIS;  
RA DONALDSON D.D., WHITTERS M.J., FITZ L., NEBEN T., FINNERTY H.,  
RA HENDERSON S.L., O'HARA R.M. JR., TURNER K.J., WOOD C.R., COLLINS M.,  
RN Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.  
RZ [3]  
R1 SEQUENCE FROM N.A.  
R2 TISSUE-BRAIN;  
RA GYO J., MINVILLE S.,  
RA Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.  
RZ [4]  
R1 FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13  
R2 (IL-13), NOT NOT TO IL-4.  
R3 -1- SUPRACELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
R4 -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
R5 -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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R3  
R4 EMBL; X5302, CAA64617.1;  
R5 EMBL; U0581, AAB1710.1;  
R6 EMBL; Y07753, CAA70021.1;  
R7 MIM: 303130;  
R8 PFM: P60304.1; fn3; 1.  
R9 PROSITE: P50340; RECEPTOR\_CYTOKINES\_2; 1.  
R0 Receptor; Transmembrane; Glycoprotein; signal.  
R1 SIGNAL 1 26  
R2 CHAIN 27 380 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN.  
R3 DOMAIN 27 343 POTENTIAL.  
R4 TRANSMEM 344 363 EXTRACELLULAR (POTENTIAL).  
R5 DOMAIN 364 380 CYTOLASMIC (POTENTIAL).  
R6 DISULFID 145 155 BY SIMILARITY.  
R7 DISULFID 184 197 BY SIMILARITY.



DB 250 EGT-RLSIOMEPVSAFPIHCFDEYEVKIHNTNGYLOIEKLMNATISIDLSKDYOV 308  
 QY 309 RSKVNYICDDGDSWMSKOCHEGDLRSKTLIRFWLPGFILLI-----VIFPTGLL 362  
 DB 309 RAAVSMCEHAGLMSWS-OPIVGNDEKRP-LREM---FVIVIMATIFILLISLI 361  
 QY 363 LRKNTYPMIP 374  
 DB 362 CRICHTMILKFP 373

RESULT 3  
 ID 1131 MOUSE STANDARD: PRT: 424 AA.  
 AC 009030:  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 15-JUL-1999 (rel. 38, Last annotation update)  
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).  
 GN IL13RA1 OR IL13RA OR IL13R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 96133964.  
 RA HILTON D.J., ZHANG J.-G., METCALF D., ALEXANDER W.S., NICOLA N.A., WILSON T.A.;  
 RA "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";  
 RA Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).  
 RT -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).  
 CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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 CC EMBL: S80963; AAB50695.1;  
 DR MGD: MGI:105052; IL13RA.  
 FT Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 424  
 FT DOMAIN 26 340 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.  
 FT TRAMSMEM 341 364 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 365 424 POTENTIAL.  
 FT DOMAIN 37 100 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 44 93 IG-LIKE C2-TYPE DOMAIN.  
 FT DISULFID 132 142 POTENTIAL.  
 FT DISULFID 171 183 BY SIMILARITY.  
 FT CARBOHYD 35 35 BY SIMILARITY.  
 FT CARBOHYD 59 59 POTENTIAL.  
 FT CARBOHYD 103 103 POTENTIAL.  
 FT CARBOHYD 136 136 POTENTIAL.  
 FT CARBOHYD 262 262 POTENTIAL.  
 FT CARBOHYD 338 338 POTENTIAL.

SEQUENCE 424 AA: 48402 MW: 1115963 CRC32:

Query Match 14.2% Score 298; DB 1; Length 424;

Best Local Similarity 25.8%; Pred. No. 3.5e-16; Matches 108; Conservative 70; Mismatches 158; Indels 82; Gaps 21;

QY 8 IGLYFETVIST-TFGCTSSSDTEIKVNPPODEIYDPGLYGLYLQWQPLSLCHKEECT 66  
 NC 7 LGELVLMLMTNTVGVAAA-e-TEVQPPVTLNLSVENVLCITIMWSPPEGAS--PNCT 61  
 QY 67 VEX-----ELKRYNGSETWKTITIKNLHYKDFGLNKIEAKIHITLPMOCT-NGSEVQ 120  
 D 62 LRYFSHLDQOQKIAPET-----HRKEELPDEKICIQVGS---QCSANESEKP 108  
 QY 121 SSWAEVYVWIS-PCGTPERKVDMDCCVYNNQYLCSKMPGIGVLDITNINLFYWEGLD 179  
 D5 109 SPLVKRC--ISPEGQEEAVTELKCIWHNLSTYMCWMLPGNRTSPDHYTLYWYSSLE 166  
 QY 180 HALQVDYVTKADQNGICGPFYLEAS---DYKDFYICVNGSSEKRPFRSSYTFPOLNTY 236  
 LC 167 KSRQC-ENYRSGQHTACFKLTKVEPSEHONVQIMVMDNAG--IRSCKIYSLTSYV 223  
 QY 237 KPYLYLFTRESCEIKLWSTPLGPIPARCFDEIEIR----- 278  
 D6 224 KPDPF-PKHLKLLKNGALLVQWKNPNQ-PRSRCLTYEVEVWNTQDRHNLVEEDKQN 281  
 QY 278 -EDYITL-----VATVENEYITLKTNETRQLOCFVRSKVNITCSDGIMSEMSDQ 329  
 DB 222 SSSDFTEGTCFQPLPGVADAVYVAVKVKTKLCE-----DNRKLSMDSEAQ 331  
 QY 330 CMEGDLRSK-TLIRFWLPGFILLIVITGLLR-KENYTP-----KMIPEFCD 379  
 DB 332 FSGPFGNSFYITMLITIV-FVAVAVITLLTYKRLKIIIPPIPDPKIRKEMGD 388

#### RESULT 4

ID 1131 HUMAN STANDARD: PRT: 427 AA.

AC P78552: 099656;  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 15-JUL-1999 (rel. 38, Last annotation update)  
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1).  
 GN IL13RA1 OR IL13RA OR IL13R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-CARCINOMA;  
 RX MEDLINE: 97165986.  
 RA MITOUB B., LAURENT P., BONNIN O., LUPKER J., CAPUT D., VITA N., FERRARA P.;  
 RA "Cloning of the human IL-13R alpha chain and reconstitution with the IL13R alpha of a human IL-4/IL-13 receptor complex.";  
 RA FEBS Lett. 401:163-166(1997).  
 FT [2]  
 FT SEQUENCE FROM N.A.  
 FT TISSUE-B-CELL;  
 FT GAUCHAT J.F.M., SCHLAGENHAUF E., FENG N.P., MOSER R., YAMAGI M., JEANIN P., AGUANI S., ELSON G., NOTARANGELO L.D., WELLS T., EUGSTER H. 2, BOURNEPOY J.Y.;  
 FT Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.  
 FT [3]  
 FT SEQUENCE FROM N.A.  
 FT TISSUE-T-CELL;  
 RX MEDLINE: 97067184.  
 RA KIAN M.J., WAYERI N., OBIRI N.I., PURI R.K., MODI W.S., LEONARD W.J.;  
 RT "CDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";

RL J. Biol. Chem. 271:29265-29270(1996).

CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-  
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN  
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA  
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF  
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.  
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,  
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,  
CC SKELETAL MUSCLE AND OVARY. LOWEST LEVELS IN BRAIN, LUNG AND  
CC KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.  
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -----  
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CC EMBL: Y10659; CAA71669.1; -  
CC EMBL: Y09328; CAA70508.1; -  
CC EMBL: U62858; AAB37127.1; -  
CC HSSP: P31785; IILN.  
CC MIM: 300119; -  
CC PFM: PFO0041; fn3; 1.  
CC Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.  
CC SIGNAL 1 21 POTENTIAL.  
CC CHAIN 22 427 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.  
CC DOMAIN 22 343 EXTRACELLULAR (POTENTIAL).  
CC TRASMEM 344 367 POTENTIAL.  
CC DOMAIN 368 427 CYTOPLASMIC (POTENTIAL).  
CC DISULFID 39 102 IS-LIKE C2-TYPE DOMAIN.  
CC DISULFID 46 95 POTENTIAL.  
CC DISULFID 134 144 BY SIMILARITY.  
CC DISULFID 173 185 BY SIMILARITY.  
CC CARBOHYD 37 37 POTENTIAL.  
CC CARBOHYD 61 61 POTENTIAL.  
CC CARBOHYD 105 105 POTENTIAL.  
CC CARBOHYD 138 138 POTENTIAL.  
CC CARBOHYD 157 157 POTENTIAL.  
CC CARBOHYD 235 235 POTENTIAL.  
CC CARBOHYD 265 265 POTENTIAL.  
CC CARBOHYD 293 293 POTENTIAL.  
CC CARBOHYD 329 329 POTENTIAL.  
CC CARBOHYD 341 341 POTENTIAL.  
CC CARBOHYD 130 130 T -> I (IN REF. 3).  
CC CONFLICT 358 358 G -> D (IN REF. 3).  
CC CONFLICT 358 358  
CC SEQUENCE 427 AA; 48759 MW; 88E33C57 CRC32;

Query Match 14.0%; Score 295.5; DB 1; Length 427;  
Best Local Similarity 26.0%; Pred. No. 5.5e-16;  
Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 11 LTFPLSTFTGCTSSDTEIKNPPDFDELVPBGYIGYLYLOMOPLSLDHRECEVER- 70  
DB 10 LWALLACAGGGGGGGAAPTEOPVTLNLSVENICCTIWMWNPBGAS--SNCSLWYF 67  
QY 70 ----ELKYNIGSETWKTITIKNLHKDGEFLNKGIKIAHTLLPQC-TNGSEVQSSWA 124  
DB 68 SHFGDQDKKIAPETRRST-----EVLNERICLVGVS---QCSINSEKPSILV 114  
QY 125 ETTYWIS-POGIPETKVQDMDCVYNNMOYLCSMKPGICVLLDTNNTNLYWYEGDLHALQ 183  
DB 115 EKC--ISPEGPEASVTELOCTIWHNLSTMKCSWLPGRNTSDINTNTLYWHRSLKTIHQ 172  
QY 184 CVDYIKAGDQNGICRPYLEASD--YKDYICVNGSSSEKPIRSSYTFQLONIYKPLPP 241

DB 173 C-ENIFREGGYGCSFDLTKYKSSFEQHSVOIMWKAGIKPSFNIVPLTSRYKPPDP 231  
QY 242 --VLTFTRESCEELKWSIPGLPIPARCFDYETIEIREDDTT-----LVTAATVENETY 293  
DE 233 HIKNISFAND---DIYOMENPONT-SRCLFYEVEVANSOTETHNHYVDEAKCENEF 287  
QY 294 TLKTNETROLCFVV-----RSKVNICY-SDDGISEWSDKQCEGEDLSRK 339  
DB 288 ERNVENTS---CFWPGVLPPTLNTVRIRVTKNKLCEYEDKLSMWQEM-----SIRKK 339  
QY 340 TLLRWLPF-----GFLIVIEFTGL-LLRKNTP-KMIPPEFD 379  
DB 340 RNSLTLYTMLIVPVIAGAILVILLIKRLKIIFPIPPDKIKEMFED 391

RESULT 5  
PRLR\_CHICK ID PRLR\_CHICK STANDARD; PRT; 831 AA.  
AC 004594;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CBRLP).  
GN PRLR.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
RN [1]  
RE SEQUENCE FROM N.A.  
RC STRAIN-WHITE LECHORN; TISSUE-KIDNEY;  
RX MEDLINE: 93075121.  
RA TANAKA M.; MEDA K.; OKUBO T.; NAKASHIMA K.;  
RT "Double antenna structure of chicken prolactin receptor deduced from  
RT the cDNA sequence."  
RT Biochem. Biophys. Res. Commun. 188:490-496(1992).  
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
CC PROLACTIN.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -----  
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CC EMBL: D13154; BAA02439.1; -  
CC PIR: J01655; JQ1655.  
CC HSSP: P16471; JBP3.  
CC PFM: PFO0041; fn3; 4.  
CC PROSITE: PS00241; RECEPTOR\_CYTOKINES\_1; 2.  
CC PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; 2.  
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
CC SIGNAL 1 23 POTENTIAL.  
CC CHAIN 24 831 PROLACTIN RECEPTOR.  
CC DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).  
CC TRASMEM 439 459 POTENTIAL.  
CC DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 123 225 FIBRONECTIN TYPE-III.  
CC DOMAIN 122 122 FIBRONECTIN TYPE-III.  
CC DOMAIN 128 325 FIBRONECTIN TYPE-III.  
CC DOMAIN 326 428 FIBRONECTIN TYPE-III.  
CC DISULFID 36 46 BY SIMILARITY.  
CC DISULFID 75 86 BY SIMILARITY.  
CC CARBOHYD 59 59 POTENTIAL.  
CC CARBOHYD 91 91 POTENTIAL.  
CC CARBOHYD 100 100 POTENTIAL.  
CC CARBOHYD 112 112 POTENTIAL.  
CC CARBOHYD 132 132 POTENTIAL.  
CC CARBOHYD 262 262 POTENTIAL.

FT CARBOHYD 303 303 POTENTIAL.  
 FT CARBOHYD 315 315 POTENTIAL.  
 FT CARBOHYD 335 335 POTENTIAL.  
 SQ SEQUENCE 831 AA: 94102 MM: B977BF07 CRC32:

Query Match 12.5%; Score 263; DB 1; Length 831;  
 Best Local Similarity 26.4%; Pred. No. 4.2e-13;  
 Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

QY 18 TTFCTSSSDTEIKV--PPQDFE-----YLGITYLQWQPPSL 59  
 DB 97 TTFNITVATNEIGSNSSDPQYDVATSIYQSPVNLLETFRSANIMYLMAKSPPLA 156  
 QY 60 DHKRECTVEYELKRYNIGSEMTKTTIKNLHYDGFNDKNGIAKIHITLLPQCTNGSEV 119  
 DB 157 DASSNHLHYELKIKPEKEEMETI--SVGVQLOCKIN--LNAGMKRYVQVCTLDPE 212  
 QY 120 QSSMAETTYWISFQG-IPETKYQDMQCVYYNMQYLLCSMKPGIGVLLDTNYNLFYWEGL 178  
 DB 213 WBSWSEERHLLIPSGSPPEKPTIKCRSEKETFTQWMPGLDGGHPTNYTLLYKEGE 272  
 QY 179 DHALQCVDTKADGONIGCRPYLEASDYKDFYICVNGSEKRPINSSYFTFOLQNIKP 238  
 DB 273 EGVYECPPDY-RTAGPN-SCYFDRKHTSFMTYINIVRATNEMGSNSDPHYVDVYIYOP 330  
 QY 239 LPVYCTFRESCEIK-----LKMS--IPGIPARCFDEIEIR---EDDTLVATFVEN 290  
 DB 331 DPEVNTLELKRPNKRPVLTWSPPLADVNSGMLTLEYELRLKPESEMETTFVGO 390  
 QY 291 ET-YLTKTNETRQLCFVYRSKVNICYSD--GIWSEMSDKQCE--GEDLSKTKLLRFWL 346  
 DB 391 QYQYKFSINPKKTY-----IQHKPDHSGMSSESENTIQLPNDRYVDMT-VWI 443  
 QY 347 PPGFT--LLLVFVVGGLLRKPNTPYKMP 374  
 DB 444 VLGVLSTLCLIMSTMVWLKGYRMIFMLP 473

## RESULT 6

IL5R\_MOUSE STANDARD: PRT: 415 AA.

AC IL5R\_MOUSE  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).  
 GN IL5RA OR IL5R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91092260.  
 RA TAKAKI S., TOMINAGA A., MITA S., SONODA E., YAMAGUCHI N.,  
 RA TAKATSU K.;  
 RT "Molecular cloning and expression of the murine interleukin-5  
 receptor."  
 RT EMBO J. 9:4367-4374(1990).  
 RL -I- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN  
 CC BINDS TO IL-5.  
 CC -I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA  
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO  
 CC ON B-CELLS.  
 CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -I- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL D90205; BAA14231.1;  
 DB PIR: S12357; S12357.  
 LR MGD: MGI:96558; IL5RA.  
 LR PROSITE: PS00241; RECEPTOR CYTOKINES\_1; FALSE\_NEG.  
 LR PROSITE: PS00340; RECEPTOR CYTOKINES\_2; 1.  
 FM Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 18 339 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 340 361 POTENTIAL.  
 FT DOMAIN 362 415 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 131 152 BY SIMILARITY.  
 FT DISULFID 179 193 BY SIMILARITY.  
 FT CARBOHYD 32 32 POTENTIAL.  
 FT CARBOHYD 128 128 POTENTIAL.  
 FT CARBOHYD 213 213 POTENTIAL.  
 FT CARBOHYD 241 241 POTENTIAL.  
 SQ SEQUENCE 415 AA: 46989 MM: 415D6A67 CRC32:

Query Match 11.7%; Score 247; DB 1; Length 415;  
 Best Local Similarity 24.6%; Pred. No. 3.2e-12;  
 Matches 91; Conservative 70; Mismatches 151; Indels 58; Gaps 18;

QY 34 PPDFIVDPGVLYLYLQWQPPSLDHRKCTVEYELKRYNIGSEMTKTTIKNLHYD 93  
 DB 29 PPNVETIKATG-LAQVLLHMDPNPQEQ--RHVDLEYHVKINAPQEDVDTRKTES---KC 83  
 QY 94 GRTNKGIAKTIITLLPQCTNGSEVQSSMAETTYWISFQIGETFTVQDMQCVYYN----- 150  
 DB 84 VYPLHGFAPASVFTLK-----SSHITLASSWVSAEL-KAPGSGISVTLNCTTHVSS 139  
 QY 150 -----WQY-LCSMKRPGIGVLLDTNYNLFYWEGLDHALQCVDTK-ADGONIGCRFP- 201  
 DB 140 HTLRLRYQVSLNCTWLVGADAPEDTQYFLYLRGVLT--KQCEYRDLNRTACMFR 197  
 QY 201 -VLEASDYKDFYICVNGSEKRPINSSYFTFOLQNIKPLPYLLTFRRESCEIKLMS 259  
 DB 198 TETNSKGFEDLAVHNGSSKRAIKRFDOLFSLAIDQVNPVNTVLEISN-SLYIOWE 256  
 QY 260 IIPGIPARCFDEIEIRDD-----TTVATVNTYNTYLLKTNETRQLCFVY 308  
 DB 257 KPLSAPDFCFNEELKTYNTRKNGHIOKEKLINKEFSKIDVSTYSIQ-----V 305  
 QY 309 RSKVNIYCSDDGIWSEMSDKQCEGEDLSKTKLLRFW---LPFGFLLLVFVGTLLR 364  
 DB 306 RAAYSSPCRMKPGKMSGS-QPIYVGR--RKSIVE-WHLVLPFACPVLLIT--SLICR 359  
 QY 365 KPNTYPRKMP 374  
 DB 350 VCHLWTRLPF 369

## RESULT 7

ENK1-MELGA

AC ENK1-MELGA STANDARD: PRT: 831 AA.

AC 091094; 091091; 091092;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).  
 GN PRLR.  
 OS Melagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 OC Neognathae; Galliformes; Meleagris; Meleagris.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97057891.



RT "interleukin-2 receptor gamma chain: a functional component of the  
 RT interleukin-7 receptor".  
 RL Science 262:1877-1880(1993).  
 RN [17]  
 RP 3D-STRUCTURE MODELING OF 57-248.  
 RX MEDLINE: 95111955.  
 RA BAMBOROUGH P., HEGGECOCK C.J., RICHARDS W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 RT modelling".  
 RL Structure 2:839-851(1994).  
 RN [8]  
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.  
 RX MEDLINE: 94130970.  
 RA DISANTO J.P., DAUTRY-VARSAT A., CERTAIN S., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "interleukin-2 (IL-2) receptor gamma chain mutations in X-linked  
 RT severe combined immunodeficiency disease result in the loss of  
 RT high-affinity IL-2 receptor binding".  
 RL Eur. J. Immunol. 24:475-479(1994).  
 RN [9]  
 RP VARIANTS XSCID LYS-68.  
 RX MEDLINE: 94375038.  
 RA MARIENWICZ S., SUBTIL A., DAUTRY-VARSAT A., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Detection of three nonsense mutations and one missense mutation in  
 RT the interleukin-2 receptor gamma chain gene in SCIDx1 that  
 RT differently affect the mRNA processing".  
 RL Genomics 21:291-293(1994).  
 RN [10]  
 RP VARIANTS XSCID HIS-162.  
 RX MEDLINE: 94300093.  
 RA ISHII N., ASAO H., KIMURA Y., TAKESHITA T., NAKAMURA M., TSUCHIYA S.,  
 RA KONNO T., MAEDA M., UCHIYAMA T., SUGAURA K.;  
 RT "Impairment of ligand binding and growth signaling of mutant IL-2  
 RT receptor gamma-chains in patients with X-linked severe combined  
 RT immunodeficiency".  
 RL J. Immunol. 153:1310-1317(1994).  
 RN [11]  
 RP VARIANTS XSCID ASN-39.  
 RX MEDLINE: 95023932.  
 RA DISANTO J.P., RIEUX-LAUCAT F., DAUTRY-VARSAT A., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X  
 RT chromosome-linked severe combined immunodeficiency with peripheral T  
 RT cells".  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).  
 RN [12]  
 RP VARIANTS XSCID CYS-226 AND HIS-226.  
 RX MEDLINE: 95397841.  
 RA PEPPER A.E., BUCKLEY R.H., SMALL T.N., PUCK J.M.;  
 RT "Two multifactorial hotspots in the interleukin-2 receptor gamma chain  
 RT gene causing human X-linked severe combined immunodeficiency".  
 RL Am. J. Hum. Genet. 57:564-571(1995).  
 RN [13]  
 RP VARIANTS XSCID SER-183.  
 RX MEDLINE: 96013903.  
 RA CLARK P.A., LESTER T., GENET S., JONES A.M., HENDRIKS R.,  
 RA LEVINSKY R.L., KINNON C.;  
 RT "Screening for mutations causing X-linked severe combined  
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand  
 RT conformation polymorphism analysis".  
 RL Hum. Genet. 96:427-432(1995).  
 RN [14]  
 RP VARIANTS XSCID GLN-HIS-TRP INS-237.  
 RX MEDLINE: 95164726.  
 RA PUCK J.M., PEPPER A.E., BEDARD P.M., LAFRANCOISE R.;  
 RT "Female germ line mosaicism as the origin of a unique  
 RT gamma-chain mutation causing X-linked severe combined  
 RT immunodeficiency".  
 RL J. Clin. Invest. 95:895-899(1995).  
 RN [15]  
 RP VARIANTS XSCID GLN-271.  
 RX MEDLINE: 95190013.

RA SCHNALEITZ F.C., LEONARD W.J., NOGUCHI M., BERG M., RUDLOFF H.E.,  
 RA DENNEY R.F., DAVE S.R., BROOKS E.G., GOLDMAN A.S.;  
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a  
 RT moderate form of X-linked combined immunodeficiency".  
 RL J. Clin. Invest. 95:1169-1173(1995).  
 RN [16]  
 RP VARIANTS XSCID ARG-115.  
 RX MEDLINE: 97042245.  
 RA STEPHAN V., WAHN V., LE DEIST F., DIRKSEN U., BROKER B.,  
 RA MULLER-FLECKENSTEIN I., HORNEFF G., SCHROTEN H., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Atypical X-linked severe combined immunodeficiency due to possible  
 RT spontaneous reversion of the genetic defect in T cells".  
 RL New Engl. J. Med. 335:1563-1567(1996).  
 RN [17]  
 RP VARIANTS XSCID GLN-285.  
 RX MEDLINE: 97295088.  
 RA JONES A.M., CLARK P.A., KATZ F., GENET S., MCMAHON C., ALTERMAN L.,  
 RA CANT A., KINNON C.;  
 RT "B-cell-negative severe combined immunodeficiency associated with a  
 RT common gamma chain mutation".  
 RL Hum. Genet. 99:677-680(1997).  
 RN [18]  
 RP VARIANTS XSCID CYS-222.  
 RX MEDLINE: 98064061.  
 RA SHARPE N., SHAHAR M., ROIFMAN C.M.;  
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus  
 RT morphology".  
 RL J. Clin. Invest. 100:3036-3043(1997).  
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF  
 CC INTERLEUKINS.  
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND  
 CC IL-13 RECEPTORS.  
 CC -1- PROBABILITY ALSO THE IL-13 RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED  
 CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE  
 CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide C0132 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/ncbi/cd/c0132.htm".  
 CC -1- DATABASE: NAME-IL2RGbase; NOTE-X-linked SCID mutation database;  
 CC WWW="http://www.nhgri.nih.gov/DIR/LGT/SCID/IL2RGbase.html".  
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 CC or send an email to [license@sdb-sdb.ch](mailto:license@sdb-sdb.ch)).  
 CC -----  
 DR EMBL: E11085; BAA01857.1;  
 DR EMBL: I12183; AAB59145.1;  
 DR EMBL: I12178; AAB59145.1; JOINED.  
 DR EMBL: I12175; AAB59145.1; JOINED.  
 DR EMBL: E12177; AAB59145.1; JOINED.  
 DR EMBL: E12179; AAB59145.1; JOINED.  
 DR EMBL: I12180; AAB59145.1; JOINED.  
 DR EMBL: I12181; AAB59145.1; JOINED.  
 DR EMBL: I12182; AAB59145.1; JOINED.  
 DR EMBL: I19546; AAC37524.1;  
 DR PIR: A42565; A42565.  
 DR PDB: 1TLM; 26-JAN-95.  
 DR YDB: 1TLM; 26-JAN-95.  
 DR KIM: 300400;  
 DR KIM: 308380;  
 DR PAM: PFO0041; fn3: 1.  
 DR PROSITE: PS00241; RECEPTOR\_CYTOKINES\_1;  
 DR PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; FALSE\_NEG.  
 DR Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;  
 CC Query Match 10.5%; Score 220; DB 1; Length 369;







RT "Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gamma chain: chromosomal mapping and tissue specificity of IL-2R gamma chain expression." [3] Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).

RM SEQUENCE FROM N.A.

RP MEDLINE: 93366191.

RA KOBAYASHI N., NAKAGAWA S., MINAMI Y., TANIGUCHI T., KONO T.; "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma." [4] Gene 130:303-304(1993).

RM SEQUENCE FROM N.A.

RP MEDLINE: 95104285.

RA DISANTO J.P., CERRAIN S., WILSON A., MACDONALD H.R., AVNER P., FISHER A., DE SAINT BASILE G.; "The murine interleukin-2 receptor gamma chain gene: organization, chromosomal localization and expression in the adult thymus." [5] Eur. J. Immunol. 24:3014-3018(1994).

RM SEQUENCE FROM N.A.

RP STRAIN-B6.S;

RC MEDLINE: 96341745.

RA CHIU R.K., DROLL A., COOPER D.L., DOUGHERTY S.T., DIRKS J.F., DOUGHERTY G.J.; "Molecular mechanisms regulating the hyaluronan binding activity of the adhesion protein CD44." J. Neurosci. 15:2319-2329(1995).

RT J. Neurosci. 15:2319-2329(1995).

CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF INTERLEUKINS.

CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND PROBABLY ALSO THE IL-13 RECEPTORS.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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CC -----

DR EMBL: D13821: BAA02974.1: -

DR EMBL: U21795: AAA64279.1: -

DR EMBL: D13565: BAA02760.1: -

DR EMBL: L20048: AAA39286.1: -

DR EMBL: S75852: AAB32904.1: -

DR EMBL: S75844: AAB32904.1: JOINED.

DR EMBL: S75845: AAB32904.1: JOINED.

DR EMBL: S75847: AAB32904.1: JOINED.

DR EMBL: S75848: AAB32904.1: JOINED.

DR EMBL: S75849: AAB32904.1: JOINED.

DR EMBL: S75850: AAB32904.1: JOINED.

DR EMBL: S75851: AAB32904.1: JOINED.

DR EMBL: X75337: CAA53085.1: -

DR PIR: J05092: J05092.

DR PIR: J05093: J05093.

DR PIR: J05094: J05094.

DR HSSP: P31785: J05094.

DR MGD: MGI:96551: IL2RG.

DR PFAM: PF00041: fn3.1.

DR PROSITE: PS00241: RECEPTOR\_CYTOKINES\_1; 1.

DR PROSITE: PS00340: RECEPTOR\_CYTOKINES\_2; FALSE\_NEG.

DR Receptor; Transmembrane; Glycoprotein; signal.

KM SIGNAL 1

FT CHAIN 22

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DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96268473.
RA YOO J., STONE R.T., SOLIMNS-TOLODO S., FRIES R., BEATTIE C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
RT gamma gene.";
RL DNA Cell Biol. 15:453-459(1996);
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTOR.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U33748; AAB07812.1; -.
CC HSSP: P31785; 11LN.
DR DR PROSITE: PS00041; fn3.1.
DR DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
KW Receptor; Transmembrane; Glycoprotein; signal.
FT FT SIGNAL 1 22
FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290 POTENTIAL.
FT DOMAIN 291 379 CYTOSOLIC (POTENTIAL).
FT DOMAIN 158 256 FIBRONECTIN TYPE-III.
FT DISULFID 68 78 POTENTIAL.
FT DISULFID 109 122 POTENTIAL.
FT CARBOHYD 77 77 POTENTIAL.
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 90 90 POTENTIAL.
FT CARBOHYD 166 166 POTENTIAL.
FT CARBOHYD 171 171 POTENTIAL.
SQ SEQUENCE 379 AA; 43037 MW; 52EFD572 CRC32;

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CIRB_HUMAN          STANDARD;          PRT;          897 AA.
10  CYR8_HUMAN
SC   P32927;
11  01-OCT-1993 (Rel. 27, Created)
12  01-FEB-1998 (Rel. 33, Last sequence update)
13  01-NOV-1997 (Rel. 35, Last annotation update)
14  CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR (CD131 ANTIGEN).
15  CSF2PB OR IL5RB OR IL3RB.
16  Homo sapiens (Human).
17  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
18  Eutheria; Primates; Catarrhini; Homiidae; Homo.
19  [1]
20  SEQUENCE FROM N.A.
21  MEDLINE: 91088571.
22  HAYASHIDA K., KITAMURA T., GOMMAN D.M., ARAI K., YOKOTA T.,
23  MITAJIMA A.
24  "Molecular cloning of a second subunit of the receptor for human
25  granulocyte-macrophage colony-stimulating factor (GM-CSF):
26  reconstruction of a high-affinity GM-CSF receptor."
27  Proc Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
28  [2]
29  REVISED TO 454.
30  RA   KITAMURA T.
31  Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
32  CC   1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
33  AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
34  CC   1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
35  CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
36  CC   1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
37  CC   1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
38  CC   1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
39  CC   1- DATABASE: NAME=PROV; NOTE=CD guide CDw131 entry;
40  WWW: http://www.ncbi.nlm.nih.gov/prow/cd/cdw131.htm
41  CC   THIS SWISS-PROT entry is copyright. It is produced through a collaboration
42  CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
43  CC   the European Bioinformatics Institute. There are no restrictions on its
44  CC   use by non-profit institutions as long as its content is in no way
45  CC   modified and this statement is not removed. Usage by and for commercial
46  CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
47  CC   or send an email to license@sib.ch).
48  -----
49  EMBL: M59941, AAA18171.1; -.
50  PIR: A39285; A39285.
51  DR   FFM: 138981; -.
52  DR   FFM: PF00041; fn3; 2.
53  DR   PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
54  DR   PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
55  KR   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
56  FT   SIGNAL 1
57  FT   CHAIN 17 897
58  FT   DOMAIN 17 443
59  FT   TRANSMEM 444 460
60  FT   DOMAIN 461 897
61  FT   DOMAIN 129 238
62  FT   DISULFID 336 434
63  FT   DISULFID 35 45
64  FT   DISULFID 75 91
65  FT   CARBOHYD 58 58
66  FT   CARBOHYD 191 191
67  FT   CARBOHYD 346 346
68  FT   SEQUENCE 897 AA; 97335 MM; AC43EASE CRC32;
69  -----
70  Query Match 8.5%; Score 178.5; DB 1; Length 897;
71  3rd Local Similarity 22.5%; Pred. No. 1,7e-06;
72  Matches 89; Conservative 57; Mismatches 144; Indels 105; Gaps 21;
73  -----
74  32 VNPDDFEIVPGYIGY-----LYLQMQP-----LSLDF----- 63
75  | | | | | | | | | | | | | | | | | | | | | | | | | | |
76  97 VLPQSFVTVDDVDFSPDPRRLGRLTVTLTQHVQPEPPDLOISTDDHFLTLTWSVAL 156
77  | | | | | | | | | | | | | | | | | | | | | | | | | | |
78  69 -----KCTVEVELKRNIGSETWK-----TITIKNLHYKGFGLNKIE-----A 103

```



GenCore version 4.5  
Copyright (c) 1993 - 1998 Compaq Inc.

OM protein - protein search, using sw model

Run on: January 20, 2000, 06:21:02 ; Search time 24.34 Seconds

(without alignments)  
956.326 Million cell updates/sec

Title: US-09-077-817-2  
Perfect score: 2104  
Sequence: 1 MAFVCAICGICLYTFLISTF.....LLRKPNTPKMIPEFCDT 380

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

Database: SPTREMBL\_11:\*

Word size: 0

Number of hits that pass the threshold: 199794

1: sp-archaea:\*

2: sp-bacteria:\*

3: sp-fungi:\*

4: sp-human:\*

5: sp-invertebrate:\*

6: sp-mammal:\*

7: sp-mhc:\*

8: sp-organellar:\*

9: sp-phage:\*

10: sp-plant:\*

11: sp-rodent:\*

12: sp-virus:\*

13: sp-vertebrate:\*

14: sp-unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194.5	56.8	383	11	088786
2	311.5	14.8	420	4	014633
3	310.5	14.8	396	4	014631
4	298.5	14.2	415	11	0920K4
5	292	13.9	333	4	015469
6	291.5	13.9	427	4	095646
7	264.5	12.6	349	6	097597
8	178	8.5	896	11	064146
9	173.5	8.2	881	13	057519
10	170	8.1	890	11	0921A0
11	165	7.8	296	6	018880
12	159	7.6	581	6	046561
13	153	7.3	217	6	046386
14	151	7.2	862	4	099665
15	151	7.2	206	4	016354
16	145.5	6.9	422	4	075462
17	142.5	6.8	410	4	014431
18	135	6.4	346	13	093404
19	133.5	6.3	333	4	016564
20	130.5	6.2	198	6	018985
21	128	6.1	874	11	P97378
22	117.5	5.6	958	4	013592
23	117.5	5.6	906	4	013593
24	117.5	5.6	896	4	013594
25	114	5.4	335	6	P79203

26	113.5	5.4	958	4	022920
27	113.5	5.4	1165	4	092921
28	113.5	5.4	896	4	092919
29	110	5.2	6875	6	028733
30	109.5	5.2	26926	4	010466
31	107.5	5.1	710	13	057520
32	107	5.1	634	6	046600
33	106	5.0	511	12	089000
34	106	5.0	511	12	089664
35	105.5	5.0	1825	5	061210
36	102	4.8	229	6	027930
37	101.5	4.8	233	4	000207
38	101	4.8	800	11	063257
39	101	4.8	511	12	088939
40	100	4.8	229	6	028206
41	100	4.8	817	13	007784
42	99.5	4.7	895	11	062960
43	98.5	4.7	1093	11	070535
44	98.5	4.7	2222	5	097394
45	98.5	4.7	2302	11	088488

## ALIGNMENTS

FEELT 1	PRELIMINARY:	PRT:	383 AA.
088786			
11-NOV-1998 (TREMBLrel. 08, Created)			
01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
IL-13 RECEPTOR ALPHA 2.			
Mus musculus (Mouse)			
Chordata: Craniata: Vertebrata: Mammalia:			
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:			
Eutheria: Rodentia: Sciurognathi: Muridae: Mus.			
SEQUENCE FROM N.A.			
STRAIN: C3H/HEJ; TISSUE: THYMUS;			
MEDLINE: 3391042;			
DONALDSON D.D., WHITTESS M.J., FITZ L., NEBEN T.Y., FINNERTY H.,			
HENDERSON S.L., O'HARA R.M. JR., BEIER D.R., TURNER K.J., WOOD C.R.,			
COLLINS M.			
The murine IL-13 receptor alpha 2: molecular cloning,			
characterization, and comparison with murine IL-13 receptor alpha			
1, Immunol. 161:2317-2324 (1998).			
FEELT 065747; AAC33240.1;			
SEQUENCE 383 AA; 44483 MW; 5EAEF3E3 CRC32;			
Query Match	56.8%;	Score 1194.5;	DB 11; Length 383;
Best Local Similarity	58.9%;	Pred. No. 4.7e-98;	
Matches: 219; Conservative: 55; Mismatches: 91; Indels: 7; Gaps: 3;			
1 MAFVCAICGICLYTFLISTF.....LLRKPNTPKMIPEFCDT 60			
1 MAFV--HICLCFLICTTIGTS-----LEIKVNPDPDFELIDGLIGYILQKPPVILE 54			
HEKCTVEYELKRYNGSESTWTKIITKRLHYKDPFLNGIEAKIHTLLPWCOTNGSEVO 120			
KFKGCTLEKRYKRVDSWTKIITRNLINDGFLNGIEAKIHTLSEKCTNGSEVO 114			
SSAETTWISPOGIPETVQDMCYIYVWQILCSWKAGIGVLDITNNLFTWYEGDLH 180			
SPITEASYISDEGSLKIDMKCIYVWQYVCSWKAGIKTYSDNTNMFWEYEGDLH 174			
AACGVYIKADQNCICRPYLEASDKPYICVNGSENKPRSSYFFQLONYKPLP 240			
KACQADYLAHDEKNVCKKSNLSDSKYKDFICVNGSSLEPRSSYTYFQLONYKPLP 234			
PVLLTFRESSECIKRWKSIPLGPIPARCFDYEIEIREDDITLVATVNEETYLKTNE 300			

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Db 225 PELHISVENSIDIRKMNSTPGPIPPRCYVEIAREDDISWESATDKNDKLRANE 294
QY 301 TROLCEVAVKNIYCCDDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILLVFTVG 360
Db 295 SDDLCFPRCKKNIYACADGIMSEMSSEECWEGYGPDSKII-FIVPVCLFIFILLILC 353
QY 361 LILKRPNTYPKM 372
Db 354 LIVEKEPEPTL 365

RESULT 2
Q14633 PRELIMINARY: PRT: 420 AA.
AC Q14633;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
RT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSIL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE; 92121815.
RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;
RT "Molecular cloning and expression of the human interleukin 5
RT receptor";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X61176; CAA43483.1; -.
KW Signal.
FT CHAIN 1 20 POTENTIAL.
FT SIGNAL 21 420 INTERLEUKIN-5 RECEPTOR.
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 420 AA; 47670 MM; 247AB980 CRC32;

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Query Match 14.8%; Score 311.5; DB 4; Length 420;
Best Local Similarity 26.9%; Pred. No. 7.9e-20;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

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QY 27 DTEIKVNPPOFEIYDPEYLGILYLOMOPPLSDHFKECTVEYELKRNISSEWTKITIT 86
Db 25 DEKISLPPVNETIKYTG-LAQVLLQMKPNPDOQ-RVNNLEYQVKINAPKEDDEYETRT 82
QY 87 KNIHKDGFEDLNKIGIEAKIHTLLPMQCTNGSEVOSSNAETTYWISPOGIPETKYODMVCV 146
Db 83 ES---KCYTILHKGSASVRILO---NDHSLASSMASAEHL-APPGSPGTSVYNLCT 135
QY 147 -----YYNQOYLL-CSMKPGIGVLLDTNLYFY---WYEGDLHALQCVDYIKAD 191
Db 136 TTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYRGSWE-----ECQEYSKDT 189
QY 192 -GONGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIYKPLPYLLFTTR 248
Db 190 LGRNACWFPPTFILSKGRDMLAVLVNGSSKHSARIPDQFLALHAIDQINPLNVTAEI 249
QY 249 ESSCEIKKMSIPLGPAPRCFDEYIEIREDDTLVTATVENETTYLTKTNETROLCFV 308
Db 250 EGT-RLSIQWKEKPVSAFPIHCFDYEKIHNTNRNGYLQIEKMTNAPFISIIDLSKYDVOV 308
QY 309 RSKVNIYCSDDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILL-----VIFVTGL 362
Db 309 RAAVSSMCREAGIMSEMS-QPIYVGNDEHKP--LREM-----FVIVMATICFILLIISLI 361
QY 363 LKRPNTYPKMTP 374
Db 362 CKICHLWIKLFP 373

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RESULT 3

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ID Q14631 PRELIMINARY: PRT: 396 AA.
AC Q14631;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
RT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.
GN HSIL5R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE; 92121815.
RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;
RT "Molecular cloning and expression of the human interleukin 5
RT receptor";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X61177; CAA43484.1; -.
KW Signal.
FT CHAIN 1 20 POTENTIAL.
FT SIGNAL 21 396 INTERLEUKIN-5 RECEPTOR TYPE 2.
FT CHAIN 21 396 INTERLEUKIN-5 RECEPTOR TYPE 2.
SQ SEQUENCE 396 AA; 44998 MM; 85FBF684 CRC32;

Query Match 14.8%; Score 310.5; DB 4; Length 396;
Best Local Similarity 26.6%; Pred. No. 9e-20;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPPOFEIYDPEYLGILYLOMOPPLSDHFKECTVEYELKRNISSEWTKITIT 86
Db 25 DEKISLPPVNETIKYTG-LAQVLLQMKPNPDOQ-RVNNLEYQVKINAPKEDDEYETRT 82
QY 87 KNIHKDGFEDLNKIGIEAKIHTLLPMQCTNGSEVOSSNAETTYWISPOGIPETKYODMVCV 146
Db 83 ES---KCYTILHKGSASVRILO---NDHSLASSMASAEHL-APPGSPGTSVYNLCT 135
QY 147 -----YYNQOYLL-CSMKPGIGVLLDTNLYFY---WYEGDLHALQCVDYIKAD 191
Db 136 TTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYRGSWE-----ECQEYSKDT 189
QY 192 -GONGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIYKPLPYLLFTTR 248
Db 190 LGRNACWFPPTFILSKGRDMLAVLVNGSSKHSARIPDQFLALHAIDQINPLNVTAEI 249
QY 249 ESSCEIKKMSIPLGPAPRCFDEYIEIREDDTLVTATVENETTYLTKTNETROLCFV 308
Db 250 EGT-RLSIQWKEKPVSAFPIHCFDYEKIHNTNRNGYLQIEKMTNAPFISIIDLSKYDVOV 308
QY 309 RSKVNIYCSDDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILL-----VIFVTGL 362
Db 309 RAAVSSMCREAGIMSEMS-QPIYVGNDEHKP--LREM-----FVIVMATICFILLIISLI 361
QY 363 LKRPNTYPKMTP 374
Db 362 CKICHLWIKLFP 373

RESULT 4
Q920K4 PRELIMINARY: PRT: 415 AA.
AC Q920K4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
RT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.
GN GPL-5RA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
RN [1]
RP SEQUENCE FROM N.A.
SQ SEQUENCE FROM N.A.

```

"Cloning and Characterization of the Guinea Pig Interleukin-5 receptor alpha cDNA."

RT Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: U55115; AAD09361.1; -

KM Signal: Receptor.

FT CHAIN 1 17 POTENTIAL.

SEQUENCE 415 AA; 46913 MW; 99EB82 CRC32;

Query Match 14.2%; Score 298.5; DB 11; Length 415;

Best Local Similarity 26.5%; Pred. No. 1.1e-18;

Matches 103; Conservative 67; Mismatches 172; Indels 47; Gaps 19;

```

OY 6 LAIGLYTFLISTFGCTSSDTEIKVNPDPDEFYDGLYLOMOPPLSLDHFKEC 65
DB 7 ILGAIETLQDTL-----PKKFLLPPIFTIKYTG-LAQVYLCEPENNQO-KNV 58
OY 66 TVEYELKRNIGSETWKIITKNLHYKDFDNLKGIKIAHTLPMQCTNGSEVOSSAE 125
DB 59 NLNHYVKINTPEEDYE--TRNTOSKCEITLHOGVSASVETIL-WH-GHSILASSWVS 112
OY 126 TTYWISPGIPTKYQDMCV-----YNNQ---YLCSMKRGISGLDITNMLEY- 174
DB 113 AEH-KAPGSGPSTIVNLCTNTAASNTNLKSYEVSLHCTWLAGKDAPEDTQYFLYR 171
OY 174 --WYEGDLHALQCVDIYKAD-GONIGCRF--YLEASDYKDFYICVNGSENKPIRSSY 227
DB 172 YGPWTE-----ECOEYSKDTLSRNTACFPFTFHSKRADLAHAVNGSSNHAITKPPD 225
OY 228 FTFOLONIYKPLPYVLTFTRESSCEIKLWSIPGLPIPARCFDEYIEI-REDDTTLVTA 286
DB 226 QLFDRQALDQPPMDVPAETEGS-RLSIQWQKPVSAFPIHCFEYEVKICNTRKYQYVER 284
OY 287 TYENETYLKTNEROLCFVYRSKVNICYSDGIMSEMSDQCMGEGELSKITLIR-FW 345
DB 285 TTTN--FVSTIDGVSKYSIOVRAANSPCRAMGIMSKMS-QPVYVKE--KKPIAGWEL 339
OY 346 LPFGFLIVFVFTGLLKRPMTPMIP 374
DB 340 ITLTAVLCFILIFFFLCRITYHLMTKMP 368

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RESULT 5

015469 PRELIMINARY: PRT: 333 AA.

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AC 015469: PRELIMINARY: PRT: 333 AA.
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PROCURSOR.
GN HSIL5R4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE: 92121815.
RA MURATA Y., TAKAKI S., MIGHTA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;
RT "Molecular cloning and expression of the human interleukin 5
RT receptor."
RL J. Exp. Med. 175:341-351(1992).
DR EMBL: X62156; CAA44081.1; -
KW SIGNAL.
FT CHAIN 1 20 POTENTIAL.
SO SEQUENCE 333 AA; 37722 MW; E86A7792 CRC32;

```

Query Match 13.9%; Score 292; DB 4; Length 333;

Best Local Similarity 28.0%; Pred. No. 3.1e-18;

Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

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OY 27 TVEYELKRNIGSETWKIITKNLHYKDFDNLKGIKIAHTLPMQCTNGSEVOSSAE 146
DB 25 DEKISLPPVNTTIKVTG-LAQVYLQWKPNDPO-RNVNLEYQKINAPKEDDETRET 82
OY 87 KNLHYKDFDNLKGIKIAHTLPMQCTNGSEVOSSAEATTYISPGIPEKRYQDMCV 146
DB 83 ES--KCVITLHKRGASASVETILQ--NDHSILASSWASAEU-APSPGTSIVNLCT 135
OY 147 -----YNNQYLL-CSMKRGISGLDITNMLEY-----WYEGDLHALQCVDIYKAD 191
DB 136 TTTEDNLSRLRSYOVSLHCTWLVGTDAPEDTQYFLYRGSWTE-----ECOEYSKDT 189
OY 192 --GONIGCRF--YLEASDYKDFYICVNGSENKPIRSSYFTFOLONIYKPLPYVLTFT 248
DB 190 LGRNIACMPREFILSKGMDLAVLVNGSSKSAIRPDLFALHALDQINPLVTAEI 249
OY 249 ESCEIKLWSIPGLPIPARCFDEYIEIREDDTTLVATVENEYTLKTNEROLCFVY 308
DB 250 EGT-RLSIQWQKPVSAFPIHCFEYEVKIHNTNGYLOJIEKLTNFIISIDLSRYQV 308
OY 309 RSKVNICYSDGIMSEMS 326
DB 309 RAAVSSKCEAGLMSWS 326

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RESULT 6

095646 PRELIMINARY: PRT: 427 AA.

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AC 095646: PRELIMINARY: PRT: 427 AA.
DT 01-MAY-1996 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC MORIMASA W., TERUMASA H.;
RT Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U81373; AAD0310.1; -
KW Receptor.
SO SEQUENCE 427 AA; 48779 MW; BED0274E CRC32;

```

Query Match 13.9%; Score 291.5; DB 4; Length 427;

Best Local Similarity 26.8%; Pred. No. 4.7e-18;

Matches 98; Conservative 59; Mismatches 139; Indels 73; Gaps 20;

```

OY 53 WQPPSLDHFKECTVEY-----ELKRNIGSETWKIITKNLHYKDFDNLKGIKIAHT 107
DB 52 WAPVVGAS--SNCSIMYTSHEGDKQDKIAPETRSI-----EYPLNERICLQVGS 100
OY 108 LIPWQ; TNGSEVOSSAEATTYIS-POGIPETKYQDMCVYNNQYLLCSMKRGISGLV 165
DB 101 ----QOSTNESKPSILYKCC--ISPEGDPESAVTELOCIHNLNLSYKCSMLPGNTPSP 154
OY 166 STYVNLFTYEGDLHALQCVDIYKADGONIGCRFPYLESD--YDFTYICVNGSENKPI 223
DB 155 PTNYLLYWHRLERLHC-ENIFREGQYFGCSFLYTKRDSFROHSQVIAWKDNAGKI 213
OY 224 RSYFTFOLONIYKPLPY-VLTFTRESSCEIKLWSIPGLPIPARCFDEYIEIREDPT 281
DB 214 KPSNIVPLTSKVPKDPPIKRLSFHND--DLIYQWENPQN-FYSRCLFYEYVANSOT 269
OY 282 T-----LVTAIVENETYLKTNEROLCFVY-----RSKVNICY-SDGI 321
DB 270 ETHNVEYVQACENDEPERVNTS--CFWVPGLPDLNTVTRIVKTNKCYEDDKL 326
OY 322 WSEMSDQCMGEGELSKITLIRFNLFP-----GFLIVIVETGL--LLKRPNTY 370
DB 327 WSNWSQEM-----SIGKRNSTLYITMLLIVPVIAGALIVLLKRLKIIIFPIIDP 381

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OY 371 - KMIEFECD 379  
DB 382 KRIKEMFGD 391

RESULT 7  
097597 PRELIMINARY; PRT; 349 AA.

AC 097597  
DT 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DE 01-MAY-1999 (TREMblrel. 10, Last annotation update)  
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
OC Bovinae; Bos.

RP [1]  
RA TRIGONA W.L., HIRANO A., BROWN W.C., ESTES D.M.;  
RT "Biological activities of interleukin-13 on bovine lymphocytes:  
implications for signaling through IL-13R $\alpha$ 1."  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF074402; AAC98147.1; -  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 349 349  
SO SEQUENCE 349 AA; 39644 MW; AB48972 CRC32;

Query Match 12.6%; Score 264.5; DB 6; Length 349;  
Best Local Similarity 24.4%; Pred. No. 9.1e-16;  
Matches 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;

OY 53 WQPLSLDHFECITYEYELKXRNISSEFWKTIITNLHYKGFDFLNKIEKIHLLRQ 112  
DB 18 WNPBGAS--PNCSTLT--FSHFENKODKTIAPET-HRSKEVPLNERICLQVGS--Q 67  
OY 113 C-TNGSEVOSSWAEETTYWISPOGIPETRYODMDCVYNNQYLCSMKRGIGVLDJTNL 171  
DB 68 CSTNESEKPSILVEKCF--SPBGDESAVTAACIMHMLRKYKWLPGRNASPPNITL 126  
OY 172 FYTEGDLHACVDYIADGONIGCRPYLEASD--YKDFIYCVNGSSSEKPPISSTFT 229  
DB 127 YWNHNSLKKILQCEFYR-EGQHICSEFNLRKXDSSEQHSVQVMDNAGKISPSFNI 185  
OY 230 FQLONIYKPLRPVILTFRESSCEIKLWSTIPGIPARCQDIETIEDDTLTATVE 289  
DB 186 VPLTSHVAP-DPSHKNLSPONGDLYVMTNQN-FQSOCLCYEVEVINSNA----- 236  
OY 290 NEYTLTKTNETR-----OLCFVY-----RSKNITVC-SPDGIMS 323  
DB 236 -ETHDIFVEEAKCONTEFEGNLEGTICFWPFGVLPDLTLNTRIVKRNKLCYEDDKIMS 294  
OY 324 EWSDKQWEGEDLSKTLRFLWLPFGFILLIVFTGLL 363  
DB 295 NWS-----QAMSIGOKANQTFYIT--TLILIPVIAAAVI 327

RESULT 8  
ID 064146 PRELIMINARY; PRT; 896 AA.  
AC 064146  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).  
GN RIL-3<BETA>.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE; 95370942.  
RA JPEL K., BUTTINI M., SAUTER A., GEBICKE-HARTER P.J.;  
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured  
microglia and its mRNA expression in vivo."  
RL J. Neurosci. 15:5800-5809(1995).

RP SEQUENCE FROM N.A.  
RC STRAIN-WISTAR; TISSUE-BRAIN;

RA GEBICKE-HARTER P.J.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; S79263; AAB35068.1; -  
DR EMBL; AJ000355; CAA04186.1; -  
DR PRAM; PF00041; fn3; 2.

FT Signal.  
FT NON\_TER 1 1  
FT NON\_TER 896 896  
SO SEQUENCE 896 AA; 99504 MW; BE7ED2CD CRC32;

Query Match 8.5%; Score 178; DB 11; Length 896;  
Best Local Similarity 21.4%; Pred. No. 1.3e-07;  
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

OY 5 CLAIGCL--YT-FLISTEGCTSSSDTEIKVN-----PQDFEIVDPGYGL 49

DB 94 CVPRCVCVLPYQFSVSKEDYSLQPDRLSIHLVPLAQHVQPPPKDISISPG--DHF 151

OY 50 YLQMPPL---SLDHFECITYEYELKXRNISSEFWKTIITNLHYKGFDFLNKIEKIH 106

DB 152 LLKMSVPLGDAQVSLSSKQDIQFEVAYKQL-QDSMED--ASSLH-----TCNLVLTLEPK 203

OY 107 TLPL-----NQTNGSEVO--SSWAEETTYWISPOGIPETRYODMDCVYNNQYL 154

DB 204 LPLPSIVAVRRAQLAPGSSLSGRGMSPEVHMDPTE-DKARNQLQCFPGIGSLN 262

OY 155 CSMPRGIGVLDITNINLFWYEGJDLHACVDYIKADGONIGCRPYLEASDYDYIYCV 214

DB 263 CSWEWTKVTDSVFGLEFYSPPRAGEKCSPVYKE-----LQASRYTRYHCSL 311

OY 215 NGSEKPKRSSTFTFOQ-----NIVKPLP-VYLTFTRESSCIRKWKSIPL 262

DB 312 NVSD--PAHSQYTVASVKRLQKGFIESFNHQMNPPTLWLTNNRS--YSLHWETOK 365

OY 263 GPIPARCDEYEIER-----EDDTLTATAVENETLTKTNETROLCEFYRSKVNICY 316

DB 366 MSYFPIQAFQVQYKKKLDREDSKT-----ENLNHAIMDLPQLEPGSYCARVAVTIP 421

OY 317 SDDGIWSEWSDKQWEGEDLSKTLRFLWLPFGFILLIVFTGLL 363

DB 422 EYKGIWSEWSEKCTWT--TDWVPTL--WI-----VLLIVELTFL 460

RESULT 9  
ID 057519 PRELIMINARY; PRT; 881 AA.

AC 057519

DT 01-JUN-1998 (TREMblrel. 06, Created)

DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)

DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)

DE GPI30P1.

GN XGP130.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;

OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;

OC Xenopus.  
RN [1]  
RA SEQUENCE FROM N.A.  
RA CHEN J., GRACE A., CHEN K.R.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF041845; AAC03531.1; -  
DR PRAM; PF00041; fn3; 4.  
SO SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;



Query Match	8.28;	Score 173.5;	DB 13;	Length 881;
Best Local Similarity	25.08;	Pred. No. 3.3e-07;		
Matches	75;	Conservative	37;	Mismatches 115;
			Indels	73;
			Gaps	14;

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OY      68 EYELKRYRNGSEYTKWTITIKNLHYKDGEDLNKGLEAKIHITLLPMOCTNGSEYQSSNAETT 127
      :|: : |:: : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      74 QYELNQRTSSVTFENLTLLN-----SPLTCNMAAGHV-----ANTL 111

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128 YMI-SPGQIETKVDMDCCVYYNMQYLLCSMKRGIGVLDITNYNLEY-W-YEGLDHALQC 184  
 112 YGIFFTLGAPPDKPTNLTCTCIYVNQDNLCTCTWDEGRPTNLPTNYITLSHRMAHFGANT- 168

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Oy 185 VDYIKADGONIGCRFPYLEASDYKDFPICVNGSSENKPIRSSYEFQLQNIYKPLPEVY - 244
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 168 -----CRGANNSCTIHSFGQFYIDTTFQVEATNELGIQKSETLTIIDPVNIYKPNPQLS 222

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244 -LIFIKESCEIENLWMSLFDGFI-----FARFIELELEBDLIVIRIVENEL 252
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 223 ELASSLEELPNALKIEWKNPIITNAFNLYKNIRYRPVKTQDMEW-VREEDT-----ASHRDS 276

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277 FTQDPLPNTVEYSIRC-----IHKDGHGFWSDWSELKQYTPRAPPSRGPDIMWK 328
D5

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RESULT	10	
0921A0		
ID	0921A0	PRELIMINARY;
		PRT; 890 AA.

DT	01-MAY-1999 (TREMBlrel. 10, Created)
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT	01-MAY-1999 (TREMBlrel. 10, Last annotation update)

GN IL5.  
OS *Cavia porcellus* (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

RN [1]  
RP SEQUENCE FROM N.A.  
RA LOGSDON N.J.; GRAHAM A.; SCOTT C.W.;  
RM "1942-43 the two reactions between the

Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
EMBL: U94688; AAC77520.1; -.  
DR  
KW  
EC  
SC

Query Match	8.1%	Score 170;	DB 11;	Length 890;
Best Local Similarity	23.8%	Pred. No. 6.8e-07;		

Matches 88; Conservative 53; Mismatches 144; Indels 84; Gaps

QY 34 PRODFEIVDFGLGYLQLQWPPSLDH---FRCTVEYELKRYRNGISFTWKTLITKNLH 90

DB 138 PRQVQINISG--DQVLIWMSVALLGPHISWDSXUJLEFEVIAKL-REPWESASI--UN 132  
QY 91 YKDG-----FDLKNIGIAKIHITLPMQCTNGSEVQ---SSWAEITYWISPOGIPETK 139

140 VODMDCVYYMMOYLLCSWPGIGVLLLTNYNLFYWEGLDHALQ-CVDYIKADGQNT--- 196

**OY** 196 -GCRPYLEASDYKDPYICVNGSSSENKPIRSSYTFQLONIWKPLPPVYLITRESSCEI 254  
| : . : : | : ||| | : : | : : | : :

```

OY      255 KKKKSIPLGPIPARCF-----DYEIEIRDDTLVTATAVENETYLK-----29
      1:1      : : :      ::1:1      : : : 111

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[illegible]

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0 297 -T AETGTCGCVMSKNVYCSDDGIMSEMSDKOCMGEGEDLSKTLRLRFV-LPGFILL 354
1 408 ATTTAT-----VAVKPSPGGATZNGINSEMSDEGRMTTD-----VALPFWIALV 452
C7 355 VIFVYVALL 363
Dc 453 LYLWV ALL 461

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```

RESULT 11
010860
ID 010860
PRELIMINARY;
PKT; 296 AA.

```

01-JAN-1998 (TREMBLrel. 05, last sequence update)  
01-NOV-1998 (TREMBLrel. 08, last annotation update)  
PROLACTIN RECEPTOR SHORT FORM.

OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae;  
CC Bovinae; Bos.  
RV [1]

F3 SCHÜTLER J. A., NAGEL R. J., GAO J., HORSEMAN N. D., KESSLER M. A.;  
KT "Prolactin receptor heterogeneity in bovine fetal and maternal  
IT tissues.";

```

LR   ENBL; AF027403; AAB83999.1; -.
DR   PRAM; PF00041; fn3; 2.
SQ   SEQUENCE   296 AA;  33854 MW;  8B40CCD8 CRC32;

```

Query Match	7.88;	Score 165;	DB 6;	Length 296;
Best Local Similarity	31.38;	Pred. NO. 4.7e-07;		
Matches	63;	Conservative	24;	Mismatches 96;
			Indels	18;
			Gaps	

136 PETKQVDMDCYYNNQYLILCSKPRGIGVLLDTNNLFYEWEGLDHALQCVDIKADGQNI 19  
 27 PPERKLVKCRSPGKEFTFCWMEPGADGLPTNTYLLTHKGEETLIHECPDY·KTGPN- 85

Db 85 SCYFSTHTSINKMYITVNAINOMGISSDPLYVHTYIYEPEPANTLTLEKHPEDRK 14

E) 145 PYLWIKWSPPTMTDVXSGWFIIQYIRLKEKAT-----DMETHFTLKQTLKIFNLIP 19  
 G) 307 VVR5KV4IYCS-DDGJNSEWS 26

## RESULT 1:

AC	046561;
D1	01-JUN-1993 (TREMBLrel. 06, Created)
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)

OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC

RY SCIENCE FROM N.A.  
 RX MEDLINE; 98001468.  
 RA PIGNON C., BINART N., ORMANDY C., SCHULER L.A., KELLY P.A.,

RT-PCR genomic analysis reveal that the two forms arise by different

alternative splicing mechanisms in ruminants and in rodents.";  
 RL J. Mol. Endocrinol. 19:109-120(1997).

RP SEQUENCE FROM N.A.  
 RA BIGNON C., DUANE J.,  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041257; AAB96795.1;  
 DR PFM: PF00041; fn3; 2.  
 KM Signal.  
 FT SIGNAL  
 FT CHAIN 1 24 POTENTIAL  
 FT SEQUENCE 581 AA; 65235 MW; 6792A7C7 CRC32; PROLACTIN RECEPTOR LONG FORM.

Query Match 7.6%; Score 159; DB 6; Length 581;  
 Best Local Similarity 27.3%; Pred. No. 3.8e-06;  
 Matches 67; Conservative 25; Mismatches 103; Indels 50; Gaps 10;

OY 136 PRTYQDMDCVYNNQYLCSSKPKGIGVLLDTNNLFYWEGLDHALQCVYIKADGQNI 195  
 DB 27 PPKFKLLIKRSPGKETFCWMEPGADGGLPNTYLLTYRKEGELLHCECPDY-KTGGPN- 85  
 OY 196 GGRFFYLEASDVKDYICVNGSSSEKPIRSSYFTQLONYKPLPPVYLTFRESSCEIK 255  
 DB 85 SCYFKKTTSTKMTVITVSALNQGSISSDPLVYDVYIVPEPPVNLTLLEKHPEDRK 144  
 OY 256 ---LKWSIP-LGPPIPARCF--DYEIEIRDDTLVATVENEYTLKTNETROLCEVY 308  
 DB 145 PYLWKMSPTLTVDKSGFISQIYEIRLKEKAT-----DDETHAPRLTDLKFNLYP 198  
 OY 309 RSK--VNITYCS-DGCIWSEMSDKOCWEGEDLSKTLRLFWLPGFILLIVIFVGLLKK 365  
 DB 199 GOKYLVQIRCKPDHGWSEMS-----PESFIQI----- 227  
 OY 366 PNTYP 370  
 DB 227 PNDP 231

## RESULT 13

OY 046386 PRELIMINARY; PRT; 217 AA.  
 AC 046386.  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
 DE PROLACTIN RECEPTOR (FRAGMENT).  
 GN PRLR.  
 OS Mustela vison (American mink).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-TESTIS.  
 RA DOUGLAS D.A., SONG J.-H., HOUE A., MURPHY B.D.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF029294; AAB88899.1;  
 DR PFM: PF00041; fn3; 1.  
 FT NON TER 1 1  
 FT SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 7.3%; Score 153; DB 6; Length 217;  
 Best Local Similarity 29.8%; Pred. No. 3.7e-06;  
 Matches 70; Conservative 26; Mismatches 87; Indels 52; Gaps 16;

OY 158 KPGIGVLLDTNNLFYWEGLDHALQCVYIKADQNGRFFYLEASDYKDYICVN-- 216  
 DB 1 KPGDGGGLPTVYLLYHKEGETTTCPCDYI-TSGPN-SCFNNKHTSIWMIYITINAT 58  
 OY 216 ---GSSEKPIRSSYFTQLONYKPLPPVYLTFRESSCEIK-----LKWSIPL 262

DB 59 NMGSSSSDP---RYVT--LRYIPEPPVNL-----SLEIKQPEDKTYLMIKM-YXP 106  
 OY 263 GPIPAR-----CFDYEIEIRDDTLVATVENEYTLKTNETROLCEVNSK--VNLYC 316  
 DB 107 TLVDYSGWLLQYETIRLKEKAT-----EWEHFAQLQCFKILSLPCOKYLVQVC 160  
 OY 317 S-DDGIWSEMSDKOCWE-GEDLSKTKTLRLFWLPGFILLI-----VIFVTGILLR 364  
 DB 161 KPDHGFSEMSKRSIQIPLNDISMKDTI-VMI-----FVAVLSAVICLINVAVALK 211

## RESULT 14

OY 099665 PRELIMINARY; PRT; 862 AA.  
 AC 099665.  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE IL-12 RECEPTOR BETA2.  
 CS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,  
 RA GATELEY M.K., GUBLER U.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U64198; AAB36675.1;  
 DR PFM: PF00041; fn3; 3.  
 FT SEQUENCE 862 AA; 97134 MW; 5FE4FB5D CRC32;

Query Match 7.2%; Score 151; DB 4; Length 862;  
 Best Local Similarity 23.8%; Pred. No. 3.2e-05;  
 Matches 73; Conservative 42; Mismatches 108; Indels 84; Gaps 17;

OY 87 KNLHYKDFDLNKGIEAKHTLTP-----NQTNGSEVQSSMAETTYWISPGIPE 137  
 DB 75 RINHHGHSINSQV-----TGLPLGTTLFVCKLACINSDEIQGAEIFVGVAPE----- 126  
 OY 138 TKVQDMDCVYNNQYLCSSKPKGIGVLLDTNNLF-----FWYSGLDHALQCVDYIK 189  
 DB 126 -QPNLSCIQKGEQVACTWGERGRDTHLYTEYTLQISGPNRLTWOK-----CKD-IY 177  
 OY 190 ADGONIGCRF-PYEASDYKDYICVN--GSSEKPIRSSYFTQLONYKPLPP--VYL 244  
 DB 178 CDYIDFGINLPESPESNFTAKTAVANSLSGSSSLP---STFT--LDIYAPLPWDIRI 232  
 OY 245 TFRRESSCEIRLKM-----SIPLEGPIPARCFDYEIEIRDDTLVATVENEYTL 295  
 DB 233 KFOKASVSRCTLYWRDEGLVLNLRKRPNSRLMN-----MVNYTKAKGRDL 281  
 OY 296 KTNETROLCEVNSKKNITYSDGCIWSEMSDK--QCWGE-----DLK 338  
 DB 282 LDKPFYEYEFQISKLHLY--KGSWSDWESLRAQTPEEPPTGMIDWYMKRHIDYSR 338  
 OY 339 KTLRLFW 345  
 DB 339 QOISLFW 345

## RESULT 15

OY 016354 PRELIMINARY; PRT; 206 AA.  
 AC 016354.  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE PROLACTIN RECEPTOR (FRAGMENT).  
 CS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]

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RP SEQUENCE FROM N.A.  
RX MEDLINE: 95286597.  
RA FUH G., WELLS J.A.;  
RT "Prolactin receptor antagonists that inhibit the growth of breast  
cancer cell lines."  
RL J. Biol. Chem. 270:13133-13137(1995).  
DR EMBL: S78505; AAB34470.1;  
PFAM: PF00041; fn3; 2.  
FT NON-TER  
SQ SEQUENCE 206 AA: 23950 MW: 17557266 CRC32;

Query Match 7.2%; Score 151; DB 4; Length 206;  
Best Local Similarity 27.9%; Pred. No. 5, 2e-06;  
Matches 58; Conservative 26; Mismatches 94; Indels 30; Gaps 9;

QY 135 IPETKYQDMDCVYYNNOYLCSNKPFGIGVLLDTNMLEFYWEGLDHALOCVDYIKADGON 194  
DB 2 LPPGKPEIFKCRSPNKETFTCMWRPFGTDGGLPTNYSILYHREGETLMHECPDYI-TGGPN 60  
QY 195 IGRFPYLEASDYKDDYICVNSSENKPIRSSYFTFQLONIIVPLRPVYLFTRESCEI 254  
DB 61 -SCHFGKQYTSMTYIMVNNATNMGSSFSDELIVDYIIVQDPPL-----ELAVEY 113  
QY 255 K-----LKWSIP-LGPIDAPCFD--YEIREDDTLVATAVENETYLKTTNET 301  
DB 114 KQPEDKKPYLMIKWSPFTLIDLKTGWFTLLXELRKP-----KAEMELHFRAGQOTEF 167  
QY 302 ROLCFYVRSK--VNIYCS-DDGIWSEWS 326  
DB 168 KILSLHPGOKYLVQVRCKPDHGYWSAWS 195

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Job time: 1004 sec

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